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OM protein - protein search, using sw model

Run on: April 18, 2006, 13:41:26 ; Search time 27 Seconds  
(without alignments)  
184.120 Million cell updates/sec

Title: US-10-764-140-4  
Perfect score: 617  
Sequence: 1 EIQLQSGPELVKPGASVQV.....RDVTALDFWGQGTTLTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.New.\*  
1: /SIDSS/ptodata/2/pubpaa/US08\_NEW\_PUB.pdb.\*  
2: /SIDSS/ptodata/2/pubpaa/US06\_NEW\_PUB.pdb.\*  
3: /SIDSS/ptodata/2/pubpaa/US07\_NEW\_PUB.pdb.\*  
4: /SIDSS/ptodata/2/pubpaa/PCT\_NEW\_PUB.pdb.\*  
5: /SIDSS/ptodata/2/pubpaa/US03\_NEW\_PUB.pdb.\*  
6: /SIDSS/ptodata/2/pubpaa/US10\_NEW\_PUB.pdb.\*  
7: /SIDSS/ptodata/2/pubpaa/US11\_NEW\_PUB.pdb.\*  
8: /SIDSS/ptodata/2/pubpaa/US60\_NEW\_PUB.pdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	617	100.0	117	US-11-087-528-4	Sequence 4, Appli
2	617	100.0	117	US-11-122-622-4	Sequence 4, Appli
3	503.5	81.6	137	US-11-074-373-39	Sequence 39, Appl
4	498.5	80.8	120	US-11-037-199-5	Sequence 5, Appli
5	483	78.3	112	US-10-246-019A-6	Sequence 6, Appli
6	468.5	75.9	139	US-10-504-389A-28	Sequence 28, Appl
7	466	75.5	118	US-11-171-567-203	Sequence 203, Appl
8	459	74.4	119	US-11-097-812-72	Sequence 72, Appl
9	459	74.4	119	US-11-097-812-81	Sequence 81, Appl
10	458	74.2	115	US-11-165-023-16	Sequence 16, Appl
11	454	73.6	119	US-11-097-812-63	Sequence 63, Appl
12	454	73.6	119	US-11-097-812-64	Sequence 64, Appl
13	454	73.6	119	US-11-097-812-65	Sequence 65, Appl
14	454	73.6	119	US-11-097-812-66	Sequence 66, Appl
15	454	73.6	119	US-11-097-812-67	Sequence 67, Appl
16	454	73.6	119	US-11-097-812-70	Sequence 70, Appl
17	454	73.6	119	US-11-097-812-71	Sequence 71, Appl
18	454	73.6	119	US-11-097-812-73	Sequence 73, Appl
19	454	73.6	119	US-11-097-812-74	Sequence 74, Appl
20	454	73.6	119	US-11-097-812-75	Sequence 75, Appl
21	454	73.6	119	US-11-097-812-76	Sequence 76, Appl
22	454	73.6	119	US-11-097-812-77	Sequence 77, Appl
23	454	73.6	119	US-11-097-812-80	Sequence 80, Appl
24	454	73.6	119	US-11-097-812-206	Sequence 206, Appl
25	454	73.6	120	US-11-097-812-136	Sequence 136, Appl

26 454 73.6 120 7 US-11-097-812-144 Sequence 144, App  
27 454 73.6 120 7 US-11-097-812-145 Sequence 145, App  
28 454 73.6 122 7 US-11-171-567-204 Sequence 204, App  
29 454 73.6 130 7 US-11-188-187A-3 Sequence 3, Appli  
30 450.5 73.0 130 7 US-11-179-820-6 Sequence 6, Appli  
31 450 72.9 115 7 US-11-165-023-31 Sequence 31, Appl  
32 450 72.9 119 7 US-11-097-812-78 Sequence 78, Appl  
33 447 72.4 115 7 US-11-165-023-32 Sequence 32, Appl  
34 447 72.4 120 7 US-11-097-812-138 Sequence 138, App  
35 447 72.4 120 7 US-11-097-812-143 Sequence 143, App  
36 445.5 72.2 671 7 US-11-202-507A-14 Sequence 14, Appl  
37 445.5 72.2 672 7 US-11-202-507A-7 Sequence 7, Appli  
38 444.5 72.0 243 6 US-10-016-686-1 Sequence 1, Appli  
39 444.5 72.0 488 6 US-10-016-686-3 Sequence 3, Appli  
40 444.5 72.0 592 6 US-10-016-686-4 Sequence 4, Appli  
41 444.5 72.0 671 7 US-11-202-507A-8 Sequence 8, Appli  
42 444.5 72.0 672 7 US-11-202-507A-6 Sequence 6, Appli  
43 443 71.8 120 7 US-11-097-812-135 Sequence 135, App  
44 441 71.5 115 7 US-11-218-813-19 Sequence 19, Appl  
45 441 71.5 119 6 US-10-507-662-22 Sequence 22, Appl

## ALIGNMENTS

## RESULT 1

US-11-087-528-4  
; Sequence 4, Application US/11087528  
; Publication No. US20050271664A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; APPLICANT: WONG, HING C.  
; APPLICANT: WEN, JING HAI  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
; TITLE OF INVENTION: OF USE THEREOF  
; FILE REFERENCE: TNA-005.06  
; CURRENT APPLICATION NUMBER: US/11/087,528  
; CURRENT FILING DATE: 2005-03-22  
; PRIOR APPLICATION NUMBER: 10/293,417  
; PRIOR FILING DATE: 2002-11-12  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: 08/814,806  
; PRIOR FILING DATE: 1997-03-10  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-087-528-4

Query Match 100.0%; Score 617; DB 7; Length 117;  
Best Local Similarity 99.1%; Pred. No. 5.9e-50;  
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 EIQLQSGPELVKPGASVQVCKTXYGFTDYNVYVWROSHGKSLWIGYIDPYNGITY 60  
Db 1 EIQLQSGPELVKPGASVQVCKTXYGFTDYNVYVWROSHGKSLWIGYIDPYNGITY 60  
QY 61 DONFKGKATLTVDKSSITAFMHLNSLTSDSDSAVYFCARDVTTLDFWGQGTTLTVSS 117  
Db 61 DONFKGKATLTVDKSSITAFMHLNSLTSDSDSAVYFCARDVTTLDFWGQGTTLTVSS 117

## RESULT 2

US-11-122-622-4  
; Sequence 4, Application US/11122622  
; Publication No. US20060039901A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; APPLICANT: WONG, HING C.  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS

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; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/11/122,622
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: US/09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-122-622-4

Query Match      100.0%; Score 617; DB 7; Length 117;
Best Local Similarity 99.1%; Pred. No. 5.9e-50;
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIQLOQSGPELVKPGASVQVSCCKTXGYSFTDYNVYVVRQSHGKSLEWIGYIDPYNGITIIY 60
Db 1 EIQLOQSGPELVKPGASVQVSCCKTXGYSFTDYNVYVVRQSHGKSLEWIGYIDPYNGITIIY 60

QY 61 DQNFKGKATLTVDKSSSTTAFMHLNSLTSDSDSAVYFCARDVTTALDFWGGGTTLTVSS 117
Db 61 DQNFKGKATLTVDKSSSTTAFMHLNSLTSDSDSAVYFCARDVTTALDFWGGGTTLTVSS 117

RESULT 3
US-11-074-373-39
; Sequence 39, Application US/11074373
; Publication No. US20060024302A1
; GENERAL INFORMATION:
; APPLICANT: Achen et al.
; TITLE OF INVENTION: CHMERIC ANTI-VEGF-D ANTIBODIES AND HUMANIZED ANTI-VEGF-D ANTIBOD
; FILE REFERENCE: 28967/39969A
; CURRENT APPLICATION NUMBER: US/11/074,373
; CURRENT FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-074-373-39

Query Match      81.6%; Score 503.5; DB 7; Length 137;
Best Local Similarity 78.8%; Pred. No. 1.8e-39;
Matches 93; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

QY 1 EIQLOQSGPELVKPGASVQVSCCKTXGYSFTDYNVYVVRQSHGKSLEWIGYIDPYNGITIIY 60
Db 20 EIQLOQSGPELVKPGASVQVSCCKTXGYSFTDYNVYVVRQSHGKSLEWIGYIDPYNGITIIY 79

QY 61 DQNFKGKATLTVDKSSSTTAFMHLNSLTSDSDSAVYFCAR-DVTTALDFWGGGTTLTVSS 117
Db 80 NQKFKGKATLTVDKSSSTTAFMHLNSLTSDSDSAVYFCARTSYGGMDYWGQGSVTVSS 137

RESULT 4
US-11-037-199-5
; Sequence 5, Application US/11037199
; Publication No. US20060030015A1
; GENERAL INFORMATION:
; APPLICANT: Japan Science and Technology Corporation
; TITLE OF INVENTION: Novel methods of producing antibody-enzyme, the antibody-enzymes,
; FILE REFERENCE: A251-01/PCT
; CURRENT APPLICATION NUMBER: US/11/037,199
; CURRENT FILING DATE: 2005-01-19
; PRIOR APPLICATION NUMBER: JP 2002-211756
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; PRIOR FILING DATE: 2002-7-19
; PRIOR APPLICATION NUMBER: JP 2002-211768
; PRIOR FILING DATE: 2002-7-19
; PRIOR APPLICATION NUMBER: JP 2003-051943
; PRIOR FILING DATE: 2003-2-27
; PRIOR APPLICATION NUMBER: JP 2003-198270
; PRIOR FILING DATE: 2003-7-17
; PRIOR APPLICATION NUMBER: JP 2003-198281
; PRIOR FILING DATE: 2003-7-17
; PRIOR APPLICATION NUMBER: JP 2003-198292
; PRIOR FILING DATE: 2003-7-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-037-199-5

Query Match      80.8%; Score 498.5; DB 7; Length 120;
Best Local Similarity 79.2%; Pred. No. 4.4e-39;
Matches 95; Conservative 11; Mismatches 11; Indels 3; Gaps 1;

QY 1 EIQLOQSGPELVKPGASVQVSCCKTXGYSFTDYNVYVVRQSHGKSLEWIGYIDPYNGITIIY 60
Db 1 EIQLOQSGPELVKPGASVQVSCCKTXGYSFTDYNVYVVRQSHGKSLEWIGYIDPYNGITIIY 60

QY 61 DQNFKGKATLTVDKSSSTTAFMHLNSLTSDSDSAVYFCAR--DVTTALDFWGGGTTLTVSS 117
Db 61 NQKFKGKATLTVDKSSSTTAFMHLNSLTSDSDSAVYFCARFVVVADVMYWGQGSVTVSS 120

RESULT 5
US-10-246-019A-6
; Sequence 6, Application US/10246019A
; Publication No. US20060073133A1
; GENERAL INFORMATION:
; APPLICANT: Kikly, Kristine K.
; APPLICANT: Abrahamson, Julie
; TITLE OF INVENTION: Sialoadhesin Factor-3 Antibodies
; FILE REFERENCE: GH50019-1C1
; CURRENT APPLICATION NUMBER: US/10/246,019A
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: USN 09/577,930
; PRIOR FILING DATE: 2000-01-22
; PRIOR APPLICATION NUMBER: USN 09/046,736
; PRIOR FILING DATE: 1998-03-24
; PRIOR APPLICATION NUMBER: USN 60/041,885
; PRIOR FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Human
US-10-246-019A-6

Query Match      78.3%; Score 483; DB 6; Length 112;
Best Local Similarity 78.4%; Pred. No. 1.1e-37;
Matches 91; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

QY 1 EIQLOQSGPELVKPGASVQVSCCKTXGYSFTDYNVYVVRQSHGKSLEWIGYIDPYNGITIIY 60
Db 1 QIQLOQSGPELVKPGASVQVSCCKTXGYSFTDYNVYVVRQSHGKSLEWIGYIDPYNDGTGY 60

QY 61 DQNFKGKATLTVDKSSSTTAFMHLNSLTSDSDSAVYFCARDVTTALDFWGGGTTLTVSS 116
Db 61 NQKFKGKATLTVDKSSSTTAFMHLNSLTSDSDSAVYFCASEGI----HWQGGTLTVSS 112

RESULT 6
US-10-504-389A-28
; Sequence 28, Application US/10504389A
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; Publication No. US20060045876A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Christoph
; APPLICANT: Scott, Andrew
; TITLE OF INVENTION: FUSION PROTEINS OF HUMANIZED G250 SPECIFIC
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
; FILE REFERENCE: LUD 5821
; CURRENT APPLICATION NUMBER: US/10/504,389A
; PRIOR FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: PCT/US03/04243
; PRIOR FILING DATE: 2002-02-12
; NUMBER OF SEQ ID NOS: 56
; SEQ ID NO 28
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: amino acid sequence for murine 19/2 heavy chain variable region
US-10-504-389A-28

Query Match 75.9%; Score 468.5; DB 6; Length 139;
Best Local Similarity 73.7%; Pred. No. 2.9e-36;
Matches 87; Conservative 15; Mismatches 15; Indels 1; Gaps 1;

QY 1 EIQLOQSGPELVKPGASVQVCKTGYSTFDYNNVYVWQSHGKSLWIGVIDPYNGITYI 60
DB 18 EVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSHGSLDWIGVIAPYSGGTG 77
QY 61 DONFKGKATLTVDKSTTAFMHLNSLTSDSAVYFCA-RDVTTLDFWQGGTTLTVSS 117
DB 78 NQEFKRAATLTVDKSSSTAYMQLKSLTSDSAVYFCARRDPFPFYDWQGGTTLRVSS 135

RESULT 7
US-11-171-567-203
; Sequence 203, Application US/11171567
; Publication No. US20060057651A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: McWhirter, John
; TITLE OF INVENTION: POLYPEPTIDES AND ANTIBODIES DERIVED FROM CHRONIC LYMPHOCTIC LEUK
; TITLE OF INVENTION: CELLS AND USES THEREOF
; FILE REFERENCE: ALEX-P06-060
; CURRENT APPLICATION NUMBER: US/11/171,567
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US 10/996,316
; PRIOR FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: US 10/894,672
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 10/736,188
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/379,151
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/US01/47931
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/254,113
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 203
; LENGTH: 118
; TYPE: PRT
; ORGANISM: murine
US-11-171-567-203

Query Match 75.5%; Score 466; DB 7; Length 118;
Best Local Similarity 72.6%; Pred. No. 4.2e-36;
Matches 85; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 1 EIQLOQSGPELVKPGASVQVCKTGYSTFDYNNVYVWQSHGKSLWIGVIDPYNGITYI 60
DB 2 EVQLQSGPELVKPGASVKISCKASGYTFDYLWVQNHGKSLWIGHIDPYGSSNY 61
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QY 61 DONFKGKATLTVDKSTTAFMHLNSLTSDSAVYFCA-RDVTTLDFWQGGTTLTVSS 117
DB 62 NLKFKGKATLTVDKSSSTAYMQLKSLTSDSAVYCGRSKRDYFDYWGQGTTLTVSS 118

RESULT 8
US-11-097-812-72
; Sequence 72, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakappagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
; TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 72
; LENGTH: 119
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-72

Query Match 74.4%; Score 459; DB 7; Length 119;
Best Local Similarity 72.3%; Pred. No. 1.8e-35;
Matches 86; Conservative 16; Mismatches 15; Indels 2; Gaps 1;

QY 1 EIQLOQSGPELVKPGASVQVCKTGYSTFDYNNVYVWQSHGKSLWIGVIDPYNGITYI 60
DB 1 EVQLQSGPELVKPGASVKISCKASGYSTGYNNMNVKQSHGKSLWIGNIDPYGGSY 60
QY 61 DONFKGKATLTVDKSTTAFMHLNSLTSDSAVYFCA-RDVTTLDFWQGGTTLTVSS 117
DB 61 NQKFKGKATLTVDKSSSTAYMQLKSLTSDSAVYFCARTATALTSTWDYWGQGTSTVTVSS 119

RESULT 9
US-11-097-812-81
; Sequence 81, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakappagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
; TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
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/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 81
/ LENGTH: 119
/ TYPE: PRT
/ ORGANISM: mouse
US-11-097-812-81

Query Match
Best Local Similarity 74.4%; Score 459; DB 7; Length 119;
Matches 86; Conservative 16; Mismatches 15; Indels 2; Gaps 1;

QY 1 EIQLOQSGPELVKPGASVQVSKTXGYSFTDYNVYVWVQSHGKSLWIGYIDPYNGITY 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLQSGPELEKPGASVKISKASGYSFTGYNMWVQKQSGKSLWIGNIDPYGDTY 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 DONFGKATLTVDKSSSTAFMHLNSLTSDSAVYFCARDVT--TALDFWQGGTTLTVSS 117
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NQKFGKATLTVDKSSSTAYMQLSLTSDSAVYVCARTATALTALSTMDYWGQGSTVTSS 119
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-11-165-023-16
/ Sequence 16, Application US/11165023
/ Publication No. US20060019342A1
/ GENERAL INFORMATION:
/ APPLICANT: Dall'Acqua, William
/ APPLICANT: Wu, Herren
/ APPLICANT: Damechroder, Melissa
/ TITLE OF INVENTION: INCREASING THE PRODUCTION OF RECOMBINANT ANTIBODIES IN MAMMALIAN
/ FILE REFERENCE: AE7000US
/ CURRENT APPLICATION NUMBER: US/11/165,023
/ CURRENT FILING DATE: 2005-06-24
/ PRIOR APPLICATION NUMBER: US 60/583,184
/ PRIOR FILING DATE: 2004-06-25
/ PRIOR APPLICATION NUMBER: US 60/624,153
/ PRIOR FILING DATE: 2004-11-02
/ NUMBER OF SEQ ID NOS: 32
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 16
/ LENGTH: 115
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: recombinant antibody variable region
US-11-165-023-16

Query Match
Best Local Similarity 74.2%; Score 458; DB 7; Length 115;
Matches 84; Conservative 17; Mismatches 14; Indels 2; Gaps 1;

QY 1 EIQLOQSGPELVKPGASVQVSKTXGYSFTDYNVYVWVQSHGKSLWIGYIDPYNGITY 60
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Db 1 EVQLQSGPELVKPGASVQVSKTXGYSFTDYNVYVWVQSHGKSLWIGYISYNGVTSY 60
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QY 61 DONFGKATLTVDKSSSTAFMHLNSLTSDSAVYFCARDVT--TALDFWQGGTTLTVSS 117
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NQKFGKATLTVDKSSSTAYMQLSLTSDSAVYFCAR--SHAMDYWGQGSTVTSS 115
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RESULT 11
US-11-097-812-63
/ Sequence 63, Application US/11097812
/ Publication No. US20050281828A1
/ GENERAL INFORMATION:
/ APPLICANT: Bowdish, Katherine S.
/ APPLICANT: Dakappagari, Naveen
/ APPLICANT: Kretz-Rommel, Anke
/ TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
/ PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
/ FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
/ CURRENT APPLICATION NUMBER: US/11/097,812
/ CURRENT FILING DATE: 2005-04-01

/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 63
/ LENGTH: 119
/ TYPE: PRT
/ ORGANISM: mouse
US-11-097-812-63

Query Match
Best Local Similarity 73.6%; Score 454; DB 7; Length 119;
Matches 85; Conservative 15; Mismatches 17; Indels 2; Gaps 1;

QY 1 EIQLOQSGPELVKPGASVQVSKTXGYSFTDYNVYVWVQSHGKSLWIGYIDPYNGITY 60
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Db 1 EVQLQSGPELEKPGASVKISKASGYSFTGYNMWVQKQSGKSLWIGNIDPYGDTY 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 DONFGKATLTVDKSSSTAFMHLNSLTSDSAVYFCARDVT--ALDFWQGGTTLTVSS 117
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NQKFGKATLTVDKSSSTAYMQLSLTSDSAVYVCARTATALTALSTMDYWGQGSTVTSS 119
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-11-097-812-64
/ Sequence 64, Application US/11097812
/ Publication No. US20050281828A1
/ GENERAL INFORMATION:
/ APPLICANT: Bowdish, Katherine S.
/ APPLICANT: Kretz-Rommel, Anke
/ APPLICANT: Dakappagari, Naveen
/ TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
/ PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
/ FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
/ CURRENT APPLICATION NUMBER: US/11/097,812
/ CURRENT FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 11/016,647
/ PRIOR FILING DATE: 2004-12-17
/ PRIOR APPLICATION NUMBER: PCT/US04/06570
/ PRIOR FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: US 60/548,385
/ PRIOR FILING DATE: 2004-02-28
/ PRIOR APPLICATION NUMBER: US 60/529,500
/ PRIOR FILING DATE: 2003-12-15
/ PRIOR APPLICATION NUMBER: US 60/451,816
/ PRIOR FILING DATE: 2003-03-04
/ NUMBER OF SEQ ID NOS: 207
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 64
/ LENGTH: 119
/ TYPE: PRT
/ ORGANISM: mouse
US-11-097-812-64

Query Match
Best Local Similarity 73.6%; Score 454; DB 7; Length 119;
Matches 85; Conservative 15; Mismatches 17; Indels 2; Gaps 1;

QY 1 EIQLOQSGPELVKPGASVQVSKTXGYSFTDYNVYVWVQSHGKSLWIGYIDPYNGITY 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLQSGPELEKPGASVKISKASGYSFTGYNMWVQKQSGKSLWIGNIDPYGDTY 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 DONFGKATLTVDKSSSTAFMHLNSLTSDSAVYFCARDVT--ALDFWQGGTTLTVSS 117
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NQKFGKATLTVDKSSSTAYMQLSLTSDSAVYVCARTATALTALSTMDYWGQGSTVTSS 119
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 18, 2006, 13:32:05 ; Search time 188 Seconds  
(without alignments)

273.443 Million cell updates/sec

Title:

US-10-764-140-4

Perfect score:

617

Sequence:

1 EQLQSGPELVKPGASVQV.....RDVTTALDFWQGTTLTVSS 117

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_21.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001s.\*  
5: Geneseq2002s.\*  
6: Geneseq2003as.\*  
7: Geneseq2003bs.\*  
8: Geneseq2004s.\*  
9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	617	100.0	117	2	Aaw71288 Human ant
2	617	100.0	117	6	Abr42700 Anti-tiss
3	617	100.0	117	6	Abr42718 Anti-tiss
4	616	99.8	117	8	Adl35005 Murine an
5	616	99.8	117	9	Adu06810 Murine H3
6	616	99.8	117	9	Adw07328 Mouse ant
7	616	99.8	117	9	Adz40939 H36.D2.B7
8	611	99.0	117	6	Abr42719 Anti-tiss
9	597	96.8	117	6	Abr42720 Anti-tiss
10	584	94.7	117	6	Abr42721 Anti-tiss
11	571	92.5	117	6	Abr42722 Anti-tiss
12	561	90.9	117	6	Abr42723 Anti-tiss
13	545	88.3	117	6	Abr42730 Anti-tiss
14	542	87.8	117	6	Abr42731 Anti-tiss
15	540	87.5	117	6	Abr42724 Anti-tiss
16	539	87.4	117	6	Abr42729 Anti-tiss
17	536	86.9	117	6	Abr42725 Anti-tiss
18	536	86.9	117	6	Abr42728 Anti-tiss
19	527	85.4	117	6	Abr42726 Anti-tiss
20	521.5	84.5	118	2	Aay52755
21	521.5	84.5	118	2	Aay52756
22	521	84.4	117	6	Abr42727 Anti-tiss
23	511.5	82.9	120	7	Abr82930 Anti-huma
24	498.5	80.8	120	8	Adi26469 Murine 14

## RESULT 1

Aaw71288

ID Aaw71288 standard; protein; 117 AA.

XX AC Aaw71288;

XX DT 10-DRC-1998 (first entry)

XX DE Human anti-tissue factor heavy chain variable region.

XX KW Human, anti-tissue factor light chain variable region; H36.D2.B7;

XX KW anti-tissue factor heavy chain variable region; inhibition; antibody;

XX KW blood coagulation; thrombosis; restenosis; thromboembolic condition;

XX KW cardiovascular; infection; neoplastic disease; clot; diagnosis.

XX OS Homo sapiens.

XX PN WO9840408-A1.

XX PD 17-SEP-1998.

XX PF 10-MAR-1998; 98WO-US004644.

XX PR 10-MAR-1997; 97US-00814806.

XX PA (SUNO-) SUNOL MOLECULAR CORP.

XX PI Wong HC, Jiao J, Nieves EL, Luepschen L;

XX DR WPI; 1998-520804/44.

XX DR N-PSDB; AAV54962.

XX PT New antibody to human tissue factor - used for, e.g. treating thrombosis

XX PT or restenosis or thromboembolic conditions associated with

XX PT cardiovascular, infectious or neoplastic disease.

XX PS Claim 12; Fig 1B; 53pp; English.

XX CC The present sequence represents the human anti-tissue factor heavy chain

XX CC variable region from an antibody that binds native human tissue factor

XX CC (TF) and does not bind non-native TF. The antibody capable of

XX CC specifically-binding-native TF may be used for inhibiting blood

XX CC coagulation and also for reducing TF levels in a mammal. The antibodies

XX CC can be used, e.g. to treat thromboses, particularly to prevent or inhibit

XX CC restenosis, or other thromboses following an invasive medical procedure,

XX CC such as arterial or cardiac surgery (e.g. angioplasty, endarterectomy,

XX CC deployment of a stent, use of catheter, graft implantation or use of an

## ALIGNMENTS

25 493 79.9 117 2 Aaw84093 Murine vi  
26 492 79.7 119 8 ADR73588 Anti-AR a  
27 492 79.7 138 8 ADR73595 Anti-AR a  
28 487 78.9 113 3 Aay44588 Mouse ant  
29 487 78.9 137 3 Aay44600 Mouse ant  
30 487 78.9 236 9 ADW95680 Mouse ant  
31 487 78.9 236 9 ADX15685 Mouse ant  
32 487 78.9 237 3 Aay44595 EgcFv#125  
33 487 78.9 243 3 Aay44596 EgcFv#125  
34 484.5 78.5 116 2 Aaw95481 Mouse der  
35 483 78.3 112 5 Aae15811 Human mab  
36 479.5 77.7 467 6 Aae38408 Mouse vir  
37 478.5 77.6 118 2 Aay52760 Anti-tiss  
38 474.5 76.9 214 6 ABP96759 TSH recep  
39 474.5 76.9 214 6 ABP96760 TSH recep  
40 473.5 76.7 116 2 Aaw39889 Heavy cha  
41 472 76.5 118 4 Aae12045 Murine an  
42 472 76.5 118 7 Aae39613 Murine 5G  
43 471.5 76.4 116 2 Aaw71882 Anti-Fas  
44 471.5 76.4 116 3 Aab12919 Anti-huma  
45 471.5 76.4 130 2 Aaw71886 Anti-Fas

CC arteriovenous shunt). The antibodies can also be used as a carrier for  
 CC drugs, particularly pharmaceuticals targeted for interaction with a blood  
 CC clot such as streptokinase, tissue plasminogen activator (t-PA) or  
 CC urokinase, or a cytotoxic agent by conjugating a suitable toxin to the  
 CC antibody. Further the antibodies can be used for treating a  
 CC thromboembolic condition associated with cardiovascular disease, an  
 CC infectious disease, a neoplastic disease or as a thrombolytic agent. The  
 CC antibodies can also be used for detection and diagnosis  
 XX  
 SQ Sequence 117 AA;

Query Match 100.0%; Score 617; DB 2; Length 117;  
 Best Local Similarity 99.1%; Pred. No. 4e-49;  
 Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVWVRQSHGKSLEWIGYIDPYNGITY 60  
 DB 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVWVRQSHGKSLEWIGYIDPYNGITY 60  
 QY 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDSAVYFCARDVTTLDFWGGGTTLTVSS 117  
 DB 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDSAVYFCARDVTTLDFWGGGTTLTVSS 117

## RESULT 2

ABR42700  
 ID ABR42700 standard; protein; 117 AA.

XX ABR42700;  
 AC ABR42700;

DT 26-AUG-2003 (first entry)

XX Anti-tissue factor antibody H36.D2.B7 VH region.

XX Tissue factor; antibody; H36.D2.B7; anticoagulant; cytostatic;  
 KW antiinflammatory; mouse.

XX Mus sp.

XX Key Location/Qualifiers

FT Region 30..35 /note= "complementarity determining region 1"  
 FT Region 50..66 /note= "complementarity determining region 2"  
 FT Misc-difference 86 /note= "apparently encoded by TATT"  
 FT Region 99..106 /note= "complementarity determining region 3"

FT WO2003037911-A2.

XX 08-MAY-2003.

PF 29-OCT-2002; 2002WO-US034727.

XX 29-OCT-2001; 2001US-0343306P.

PR 21-NOV-2001; 2001US-00990586.

XX (SUNO-) SUNOL MOLECULAR CORP.

XX Jiao J, Wong HC, Nieves EL, Mosquera LA;

XX WPI; 2003-468399/44.

DR N-PSDB; ACC58569.

XX New humanized antibody that binds specifically to human tissue factor,  
 PT useful for in vivo diagnostic methods, or for inhibiting blood  
 PT coagulation or blood clot formation, angiogenesis, tumor metastases or  
 PT inflammation in a mammal.

XX Example 1; Fig 1B; 110pp; English.

XX The present sequence is the protein sequence of the heavy chain variable

CC region (VH) of anti-recombinant human tissue factor (TF) murine antibody  
 CC H36.D2.B7 (ATCC HB-12255). The invention relates to antibodies,  
 CC especially humanized H36.D2.B7, that provide superior anticoagulant  
 CC activity by binding native human TF with high affinity and specificity.  
 CC The antibodies bind human TF, either alone or present in a TF:Factor VIIa  
 CC complex, effectively preventing Factor X (or Factor IX) binding to TF or  
 CC the complex, and thereby reducing blood coagulation. The humanized  
 CC antibodies are useful for inhibiting blood coagulation or blood clot  
 CC formation, angiogenesis, tumour metastases or inflammation in a mammal.  
 CC They are also useful as drug carriers, as cytotoxic agents, for reducing  
 CC TF levels in mammals, and for in vivo diagnosis  
 XX  
 SQ Sequence 117 AA;

Query Match 100.0%; Score 617; DB 6; Length 117;

Best Local Similarity 99.1%; Pred. No. 4e-49; Mismatches 1; Indels 0; Gaps 0;  
 Matches 116; Conservative 0;

QY 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVWVRQSHGKSLEWIGYIDPYNGITY 60

DB 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVWVRQSHGKSLEWIGYIDPYNGITY 60

QY 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDSAVYFCARDVTTLDFWGGGTTLTVSS 117

DB 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDSAVYFCARDVTTLDFWGGGTTLTVSS 117

## RESULT 3

ABR42718

ID ABR42718 standard; protein; 117 AA.

XX ABR42718;  
 AC ABR42718;

DT 26-AUG-2003 (first entry)

XX Anti-tissue factor chimeric antibody ch36 VH region.

XX Tissue factor; humanization; antibody; anticoagulant; cytostatic;  
 KW antiinflammatory; mouse.

XX Mus sp.

XX Key Location/Qualifiers

FT Region 1..30 /note= "framework 1"  
 FT Region 31..35 /note= "complementarity determining region 1"  
 FT Region 36..49 /note= "framework 2"  
 FT Region 50..66 /note= "complementarity determining region 2"  
 FT Region 67..98 /note= "framework 3"  
 FT Region 99..106 /note= "complementarity determining region 3"  
 FT Region 107..117 /note= "framework 4"

PN WO2003037911-A2.

XX 08-MAY-2003.

XX 29-OCT-2002; 2002WO-US034727.

XX 29-OCT-2001; 2001US-0343306P.

PR 21-NOV-2001; 2001US-00990586.

XX (SUNO-) SUNOL MOLECULAR CORP.

XX Jiao J, Wong HC, Nieves EL, Mosquera LA;

XX WPI; 2003-468399/44.



PT New humanized antibody that binds specifically to human tissue factor,  
 PT useful for in vivo diagnostic methods, or for inhibiting blood  
 PT coagulation or blood clot formation, angiogenesis, tumor metastases or  
 PT inflammation in a mammal.

XX Claim 12; Fig 13; 110pp; English.

XX The present sequence is the protein sequence of the heavy chain variable  
 CC region (VH) of anti-recombinant human tissue factor (TF) mouse-human  
 CC chimeric antibody CH36. This sequence has been humanized in a series of  
 CC steps (see ABR42719-34) to provide a humanized VH sequence for use in the  
 CC production of an anti-human TF humanized antibody. Humanized antibodies  
 CC of the invention provide superior anticoagulant activity by binding  
 CC native human TF with high affinity and specificity. The antibodies bind  
 CC human TF, either alone or present in a TF:Factor VIIa complex,  
 CC effectively preventing Factor X (or Factor IX) binding to TF or the  
 CC complex, and thereby reducing blood coagulation. The humanized antibodies  
 CC are useful for inhibiting blood coagulation or blood clot formation,  
 CC angiogenesis, tumour metastases or inflammation in a mammal. They are  
 CC also useful as drug carriers, as cytotoxic agents, for reducing TF levels  
 CC in mammals, and for in vivo diagnosis

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 617; DB 6; Length 117;  
 Best Local Similarity 99.1%; Pred. No. 4e-49; Mismatches 1; Indels 0; Gaps 0;  
 Matches 116; Conservative 0;

QY 1 EIQLQSGPGLVKPGASVQVCKTGYSTFDYVYVWVRSQSHGKSLWIGYIDPYNGITIY 60  
 |||||  
 Db 1 EIQLQSGPGLVKPGASVQVCKTGYSTFDYVYVWVRSQSHGKSLWIGYIDPYNGITIY 60  
 |||||  
 QY 61 DQNFKGKATLTVDKSTTAPMHLNSLTSDSAVYFCARDVTTLDFWGQGTTLTVSS 117  
 |||||  
 Db 61 DQNFKGKATLTVDKSTTAPMHLNSLTSDSAVYFCARDVTTLDFWGQGTTLTVSS 117  
 |||||

RESULT 4

ADL35005  
 ID ADL35005 standard; protein; 117 AA.

XX ADL35005;

XX 03-JUN-2004 (first entry)

XX Murine anti-tissue factor heavy chain antibody protein SegID 4.

XX murine; mouse; humanised antibody; variable domain; framework region; FR;  
 KW huFR; immune system molecule; H36.D2.B7; anti-tissue factor.

XX Mus sp.

XX Key Location/Qualifiers

FT Misc-difference 25 /note= "Encoded by TCT"

XX WO2004020579-A2.

XX 11-MAR-2004.

XX 06-AUG-2003; 2003WO-US024637.

XX 29-AUG-2002; 2002US-00230880.

XX (SUNO-) SUNOL MOLECULAR CORP.

XX Wong HC, Stinson JR, Mosquera LA;

XX WPI; 2004-239169/22.

XX N-PSDB; ADL35004.

XX Producing humanized antibodies for diagnostic and therapeutic purposes

PT comprises optimizing similarity between individual antibody framework

PT regions to help identify human framework regions suitable for making the  
 PT antibodies.

XX Disclosure; SEQ ID NO 4; 137pp; English.

XX This invention relates to a novel method for producing a humanised  
 CC antibody variable (V) domain or its fragment by optimising sequence  
 CC similarity between individual antibody framework regions (FRs) in order  
 CC to identify suitable human FRs (huFRs). Specifically, it refers to novel  
 CC immune system molecules i.e. humanised monoclonal antibodies that exhibit  
 CC suitable binding affinity with reduced immunogenicity in humans. The  
 CC present invention describes a method of mutagenising DNA of non-human FRs  
 CC to encode humanised FRs having an amino acid sequence that is  
 CC substantially identical to the selected human FR previously identified  
 CC through sequence similarity searching. As such, this method provides  
 CC humanised light or heavy chain V domains of the sequence huFR1-CDR1-huFR2  
 CC -CDR2-huFR3-CDR3-huFR4, which can be used as therapeutic or diagnostic  
 CC products to treat and/or diagnose diseases in humans and animals.  
 CC Furthermore, the method expands the number of best fit possibilities that  
 CC can be generated and provides a rational basis for assembling nearly all  
 CC humanised immune system molecules of interest. This polypeptide sequence  
 CC is a murine anti-tissue factor heavy chain antibody H36.D2.B7 protein of  
 CC the invention.

XX SQ Sequence 117 AA;

Query Match 99.8%; Score 616; DB 8; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 5e-49;  
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIQLQSGPGLVKPGASVQVCKTGYSTFDYVYVWVRSQSHGKSLWIGYIDPYNGITIY 60  
 |||||  
 Db 1 EIQLQSGPGLVKPGASVQVCKTGYSTFDYVYVWVRSQSHGKSLWIGYIDPYNGITIY 60  
 |||||  
 QY 61 DQNFKGKATLTVDKSTTAPMHLNSLTSDSAVYFCARDVTTLDFWGQGTTLTVSS 117  
 |||||  
 Db 61 DQNFKGKATLTVDKSTTAPMHLNSLTSDSAVYFCARDVTTLDFWGQGTTLTVSS 117  
 |||||

RESULT 5

ADU06810

ID ADU06810 standard; protein; 117 AA.

XX ADU06810;

XX 10-FEB-2005 (first entry)

XX Murine H36.D2.B7 antibody VH SEQ ID NO:4.

XX septic shock syndrome; tissue factor; antibacterial; immunosuppressive;  
 KW antibody; antibody therapy.

XX Mus musculus.

XX Key Location/Qualifiers

FT Misc-difference 25 /note= "Encoded by TCT"  
 FT /note= "Variable amino acid"

FT Region 30..35 /label= CDR1

FT Region 50..66 /label= CDR2

FT Region 99..106 /label= CDR3

XX US2004229282-A1.

XX 18-NOV-2004.

XX 22-JAN-2004; 2004US-00764140.

XX 10-MAR-1997; 97US-00814806.

XX 16-APR-1999; 99US-00293854.

```

PR 12-NOV-2002; 2002US-00293417.
XX (SUNO-) SUNOL MOLECULAR CORP.
PA Wong HC, Jiao J;
XX WPI; 2004-813246/80.
DR N-PSDB; ADU06809.
XX
PT Treating or preventing septic shock syndrome in mammal, involves
PT administering antibody that binds native human tissue factor and does not
PT substantially bind non-native tissue factor.
XX
PS Claim 44; SEQ ID NO 4; 28pp; English.
XX
CC The invention relates to a novel method for treating or preventing (M1)
CC septic shock syndrome in a mammal, involving administering to the mammal
CC an effective amount of an antibody that binds native human tissue factor
CC and does not substantially bind non-native tissue factor, where the
CC factor X binding to the complex is inhibited and the administration is
CC sufficient to prevent or treat the septic shock syndrome in the mammal.
CC In (M1), the antibody has the binding specificity for native human tissue
CC factor about equal to or greater than H36.D2.B7 (ATCC HB-12255), and is a
CC monoclonal chimeric antibody. An antibody of the invention has
CC antibacterial and immunosuppressive activity, and acts as an inhibitor of
CC binding between factor X or factor VIIa and tissue factor/factor VIIa
CC complex. The present sequence represents the heavy chain variable region
CC of the murine antibody of the invention, H36.D2.B7.
XX
SQ Sequence 117 AA;
    Query Match          99.8%; Score 616; DB 8; Length 117;
    Best Local Similarity 100.0%; Pred. No. 5e-49;
    Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIQLOQSGPELVKPGASVQVSKTXGYSFTDYNVYVWRQSHGKSLIEWIGYIDPYNGITIY 60
DB 1 EIQLOQSGPELVKPGASVQVSKTXGYSFTDYNVYVWRQSHGKSLIEWIGYIDPYNGITIY 60
QY 61 DQNFPGKATLTVDKSSITAFMHLNSLTSDDSAVYFCARDVTTALDFWQGGTTLTVSS 117
DB 61 DQNFPGKATLTVDKSSITAFMHLNSLTSDDSAVYFCARDVTTALDFWQGGTTLTVSS 117
RESULT 6
ADW07328
ID ADW07328 standard; protein; 117 AA.
AC ADW07328;
XX
DT 07-APR-2005 (first entry)
XX
DE Mouse anti-tissue factor antibody H36.D2.B7 VH.
XX
KW Blood-clotting; heavy chain variable region; inflammation;
KW antiinflammatory; antibody; tissue factor; sepsis;
KW disseminated intravascular coagulation; anticoagulant;
KW hematological disease; thrombosis; lung injury; respiratory-gen.;
KW respiratory distress syndrome; immunosuppressive; Antibacterial;
KW Antiarthritic; Antianemic; anemia; rheumatoid arthritis;
KW glomerulonephritis; multiple sclerosis; psoriasis; sjogren's syndrome;
KW inflammatory bowel disease.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 25 /label= UNKNOWN
FT /note= "Encoded by TCT"
XX
FN WO2005004793-A2.
XX
PD 20-JAN-2005.

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XX 04-JUN-2004; 2004WO-US017900.
XX
XX 19-JUN-2003; 2003US-0480254P.
PR 22-JAN-2004; 2004US-0538892P.
XX
XX (SUNO-) SUNOL MOLECULAR CORP.
XX
XX Jiao J, Wong HC, Egan JO;
XX
XX WPI; 2005-091964/10.
DR N-PSDB; ADM07327.
XX
PT Preventing or treating sepsis or inflammation in mammals comprises
PT administering a humanized or chimeric antibody that binds to a human
PT tissue factor to form a complex in which factor X or IX binding to the
PT complex is inhibited.
XX
XX Disclosure; SEQ ID NO 4; 109pp; English.
XX
CC The invention relates to preventing or treating a sepsis or inflammatory
CC disease in a mammal comprising administering to the mammal a therapeutic
CC amount of at least one humanized antibody, chimeric antibody, or their
CC fragment that binds specifically to tissue factor (TF) to form a complex,
CC where factor X or IX binding to the complex is inhibited and the
CC administration prevents or treats the sepsis in the mammal. Also included
CC are a kit for performing the above method and reducing an inflammatory
CC cytokine production in a mammal. The inflammatory disease is associated
CC with arthritis (preferably rheumatoid arthritis), glomerulonephritis,
CC multiple sclerosis, psoriasis, Sjogren's syndrome, or inflammatory bowel
CC disease. The method also treats or prevents a sepsis-induced anemia or a
CC sepsis-related condition in a mammal, where the sepsis-related condition
CC is DIC, fibrin deposition, thrombosis, lung injury, or sepsis-associated
CC renal disorder. The lung injury is acute lung injury (ALI) or acute
CC respiratory distress syndrome (ARDS). The sepsis-associated renal
CC disorder is acute tubular necrosis. The methods and kit are useful for
CC preventing or treating sepsis or sepsis-related conditions (e.g. DIC or
CC anemia) or inflammatory diseases (e.g. arthritis). The humanized
CC antibodies are based on the chimeric antibody ch36 which comprises the
CC light and heavy chain variable regions (VL or VH) of an anti-TF antibody
CC fused to the human IgG4 heavy and kappa light constant regions. The CDRA
CC (complementarity determining region) and FR4 (framework regions) are then
CC humanized. The present sequence represents the light or heavy chain
CC variable region of the anti-TF antibody (wild-type).
XX
SQ Sequence 117 AA;
    Query Match          99.8%; Score 616; DB 9; Length 117;
    Best Local Similarity 100.0%; Pred. No. 5e-49;
    Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIQLOQSGPELVKPGASVQVSKTXGYSFTDYNVYVWRQSHGKSLIEWIGYIDPYNGITIY 60
DB 1 EIQLOQSGPELVKPGASVQVSKTXGYSFTDYNVYVWRQSHGKSLIEWIGYIDPYNGITIY 60
QY 61 DQNFPGKATLTVDKSSITAFMHLNSLTSDDSAVYFCARDVTTALDFWQGGTTLTVSS 117
DB 61 DQNFPGKATLTVDKSSITAFMHLNSLTSDDSAVYFCARDVTTALDFWQGGTTLTVSS 117
RESULT 7
ADZ40939
ID ADZ40939 standard; protein; 117 AA.
XX
AC ADZ40939;
XX
XX 14-JUL-2005 (first entry)
XX
DE H36.D2.B7 anti-tissue factor heavy chain variable region.
XX
KW antibody; tissue factor; blood-clotting; anticoagulant; vasotropic;
KW thrombolytic; cardiovascular disease; infectious disease; neoplasm;
KW thrombosis; restenosis; heavy chain variable region.
KW

```



CC complex, and thereby reducing blood coagulation. The humanized antibodies  
 CC are useful for inhibiting blood coagulation or blood clot formation.  
 CC angiogenesis, tumour metastases or inflammation in a mammal. They are  
 CC also useful as drug carriers, as cytotoxic agents, for reducing TF levels  
 CC in mammals, and for in vivo diagnosis

SQ Sequence 117 AA;  
 Query Match 99.0%; Score 611; DB 6; Length 117;  
 Best Local Similarity 97.4%; Pred. No. 1.4e-48;  
 Matches 114; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIQLQSGPELVKPGASVQVSKTXGYSTFDTNYYVWRQSHGKSLWIGYIDPYNGITY 60  
 :|||||  
 Db 1 QIQLQSGPELVKPGASVQVSKTSGYSTFDTNYYVWRQSHGKSLWIGYIDPYNGITY 60.  
 :|||||

QY 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDSNAVYFCARDVTALDFWGGGTLTVSS 117  
 :|||||  
 Db 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDSNAVYFCARDVTALDFWGGGTLTVSS 117  
 :|||||

## RESULT 9

ABR42720  
 ID ABR42720 standard; protein; 117 AA.

XX ABR42720;

XX 26-AUG-2003 (first entry)

DE Anti-tissue factor humanized antibody VH region HC-02.

XX Tissue factor; humanization; antibody; anticoagulant; cytostatic;  
 KW antiinflammatory; human; mouse.

XX Mus sp.

OS Homo sapiens.

OS Chimeric.

FX Key Location/Qualifiers  
 FT Region 1..30  
 FT /note= "framework 1"

FT Misc-difference 1  
 FT /note= "wild-type Glu substituted by Gln"  
 FT Region 31..35  
 FT /note= "complementarity determining region 1"

FT Region 36..49  
 FT /note= "framework 2"

FT Misc-difference 41  
 FT /note= "wild-type His substituted by Pro"

FT Misc-difference 44  
 FT /note= "wild-type Ser substituted by Gly"

FT Region 50..66  
 FT /note= "complementarity determining region 2"

FT Region 67..98  
 FT /note= "framework 3"

FT Region 99..106  
 FT /note= "complementarity determining region 3"

FT Region 107..117  
 FT /note= "framework 4"

FT Misc-difference 113  
 FT /note= "wild-type Leu substituted by Val"

XX WO2003037911-A2.

XX 08-MAY-2003.

XX 29-OCT-2002; 2002WO-US034727.

XX 29-OCT-2001; 2001US-0343306P.

XX 21-NOV-2001; 2001US-00990586.

XX (SUNO-) SUNOL MOLECULAR CORP.

XX

PI Jiao J, Wong HC, Nieves EL, Mosquera LA;

XX WPI; 2003-468399/44.

XX New humanized antibody that binds specifically to human tissue factor,  
 FT useful for in vivo diagnostic methods, or for inhibiting blood  
 FT coagulation or blood clot formation, angiogenesis, tumor metastases or  
 FT inflammation in a mammal.

XX Claim 12; Fig 13; 110pp; English.

XX The present sequence is the protein sequence of a humanized version, HC-  
 CC 02, of the heavy chain variable region (VH) of anti-recombinant human  
 CC tissue factor (TF) mouse-human chimeric antibody ch36. A series of PCR  
 CC mutagenesis steps was used to introduce mutations into the ch36 sequence  
 CC to fully humanize the VH region (see ABR42719-31) and hence for the  
 CC production of an anti-human TF humanized antibody. Humanized antibodies  
 CC of the invention provide superior anticoagulant activity by binding  
 CC native human TF with high affinity and specificity. The antibodies bind  
 CC human TF, either alone or present in a TF:Factor VIIa complex,  
 CC effectively preventing Factor X (or Factor IX) binding to TF or the  
 CC complex, and thereby reducing blood coagulation. The humanized antibodies  
 CC are useful for inhibiting blood coagulation or blood clot formation,  
 CC angiogenesis, tumor metastases or inflammation in a mammal. They are  
 CC also useful as drug carriers, as cytotoxic agents, for reducing TF levels  
 CC in mammals, and for in vivo diagnosis

SQ Sequence 117 AA;

Query Match 96.8%; Score 597; DB 6; Length 117;  
 Best Local Similarity 95.7%; Pred. No. 2.8e-47;  
 Matches 112; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIQLQSGPELVKPGASVQVSKTXGYSTFDTNYYVWRQSHGKSLWIGYIDPYNGITY 60  
 :|||||  
 Db 1 QIQLQSGPELVKPGASVQVSKTSGYSTFDTNYYVWRQSHGKSLWIGYIDPYNGITY 60  
 :|||||

QY 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDSNAVYFCARDVTALDFWGGGTLTVSS 117  
 :|||||  
 Db 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDSNAVYFCARDVTALDFWGGGTLTVSS 117  
 :|||||

## RESULT 10

ABR42721  
 ID ABR42721 standard; protein; 117 AA.

XX ABR42721;

XX 26-AUG-2003 (first entry)

DE Anti-tissue factor humanized antibody VH region HC-03.

XX Tissue factor; humanization; antibody; anticoagulant; cytostatic;  
 KW antiinflammatory; mouse; human.

XX Mus sp.

OS Homo sapiens.

OS Chimeric.

FX Key Location/Qualifiers  
 FT Region 1..30  
 FT /note= "framework 1"

FT Misc-difference 1  
 FT /note= "wild-type Glu substituted by Gln"

FT Region 31..35  
 FT /note= "complementarity determining region 1"

FT Region 36..49  
 FT /note= "framework 2"

FT Misc-difference 41  
 FT /note= "wild-type His substituted by Pro"

FT Misc-difference 44  
 FT /note= "wild-type Ser substituted by Gly"

FT Region 50..66

FT Region /note= "complementarity determining region 2"  
 FT 67..98  
 FT /note= "framework 3"  
 FT Misc-difference 87  
 FT /note= "wild-type Thr substituted by Arg"  
 FT Misc-difference 89  
 FT /note= "wild-type Asp substituted by Glu"  
 FT Misc-difference 91  
 FT /note= "wild-type Ser substituted by Thr"  
 FT Region 99..106  
 FT /note= "complementarity determining region 3"  
 FT Region 107..117  
 FT /note= "framework 4"  
 FT Misc-difference 113  
 FT /note= "wild-type Leu substituted by Val"  
 FT  
 XX WO2003037911-A2.  
 XX  
 XX  
 XX  
 XX 08-MAY-2003.  
 XX  
 XX 29-OCT-2002; 2002WO-US034727.  
 XX  
 XX 29-OCT-2001; 2001US-0343306P.  
 XX 21-NOV-2001; 2001US-00990586.  
 XX  
 XX (SUNO-) SUNOL MOLECULAR CORP.  
 XX  
 XX Jiao J, Wong HC, Nieves EL, Mosquera LA;  
 XX WPI; 2003-468399/44.  
 XX  
 XX New humanized antibody that binds specifically to human tissue factor,  
 PT useful for in vivo diagnostic methods, or for inhibiting blood  
 PT coagulation or blood clot formation, angiogenesis, tumor metastases or  
 PT inflammation in a mammal.  
 XX  
 XX Claim 12; Fig 13; 110pp; English.  
 XX  
 XX The present sequence is the protein sequence of a humanized version, HC-  
 CC 03, of the heavy chain variable region (VH) of anti-recombinant human  
 CC tissue factor (TF) mouse-human chimeric antibody ch36. A series of PCR  
 CC mutagenesis steps was used to introduce mutations into the ch36 sequence  
 CC to fully humanize the VH region (see ABR42719-31) and hence for the  
 CC production of an anti-human TF humanized antibody. Humanized antibodies  
 CC of the invention provide superior anticoagulant activity by binding  
 CC native human TF with high affinity and specificity. The antibodies bind  
 CC human TF, either alone or present in a TF:Factor VIIa complex,  
 CC effectively preventing Factor X (or Factor IX) binding to TF or the  
 CC complex, and thereby reducing blood coagulation. The humanized antibodies  
 CC are useful for inhibiting blood coagulation or blood clot formation,  
 CC angiogenesis, tumor metastases or inflammation in a mammal. They are  
 CC also useful as drug carriers, as cytotoxic agents, for reducing TF levels  
 CC in mammals, and for in vivo diagnosis  
 XX  
 XX Sequence 117 AA;  
 SQ  
 Query Match 94.7%; Score 584; DB 6; Length 117;  
 Best Local Similarity 93.2%; Pred. No. 4.4e-46;  
 Matches 109; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 ETLOQSGPELVKPGASVQVSKTGYSTFDNVVWVRSQSHKSLWIGYIDPYNGITY 60  
 DB 1 QILOQSGPELVKPGASVQVSKTGYSTFDNVVWVRSQSHKSLWIGYIDPYNGITY 60  
 QY 61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDSAVYFCARDVTTLDPFWGGTTLTVSS 117  
 DB 61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDSAVYFCARDVTTLDPFWGGTTLTVSS 117

RESULT 11  
 ABR42722  
 ID ABR42722 standard; protein; 117 AA.  
 XX

AC ABR42722;  
 XX  
 XX 26-AUG-2003 (first entry)  
 XX  
 XX Anti-tissue factor humanized antibody VH region HC-04.  
 XX  
 XX Tissue factor; humanization; antibody; anticoagulant; cytostatic;  
 KW antinflammatory; mouse; human.  
 XX  
 XX Mus sp.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX  
 XX Key Location/Qualifiers  
 FT Region 1..30  
 FT /note= "framework 1"  
 FT Misc-difference 1  
 FT /note= "wild-type Glu substituted by Gln"  
 FT Region 31..35  
 FT /note= "complementarity determining region 1"  
 FT Region 36..49  
 FT /note= "framework 2"  
 FT Misc-difference 41  
 FT /note= "wild-type His substituted by Pro"  
 FT Misc-difference 44  
 FT /note= "wild-type Ser substituted by Gly"  
 FT Region 50..66  
 FT /note= "complementarity determining region 2"  
 FT Region 67..98  
 FT /note= "framework 3"  
 FT Misc-difference 82  
 FT /note= "wild-type His substituted by Glu"  
 FT Misc-difference 84  
 FT /note= "wild-type Asn substituted by Ser"  
 FT Misc-difference 87  
 FT /note= "wild-type Thr substituted by Arg"  
 FT Misc-difference 89  
 FT /note= "wild-type Asp substituted by Glu"  
 FT Misc-difference 91  
 FT /note= "wild-type Ser substituted by Thr"  
 FT Region 99..106  
 FT /note= "complementarity determining region 3"  
 FT Region 107..117  
 FT /note= "framework 4"  
 FT Misc-difference 113  
 FT /note= "wild-type Leu substituted by Val"  
 XX  
 XX WO2003037911-A2.  
 XX  
 XX 08-MAY-2003.  
 XX  
 XX 29-OCT-2002; 2002WO-US034727.  
 XX  
 XX 29-OCT-2001; 2001US-0343306P.  
 XX 21-NOV-2001; 2001US-00990586.  
 XX  
 XX (SUNO-) SUNOL MOLECULAR CORP.  
 XX  
 XX Jiao J, Wong HC, Nieves EL, Mosquera LA;  
 XX WPI; 2003-468399/44.  
 XX  
 XX New humanized antibody that binds specifically to human tissue factor,  
 PT useful for in vivo diagnostic methods, or for inhibiting blood  
 PT coagulation or blood clot formation, angiogenesis, tumor metastases or  
 PT inflammation in a mammal.  
 XX  
 XX Claim 12; Fig 13; 110pp; English.  
 XX  
 XX The present sequence is the protein sequence of a humanized version, HC-  
 CC 04, of the heavy chain variable region (VH) of anti-recombinant human  
 CC tissue factor (TF) mouse-human chimeric antibody ch36. A series of PCR  
 CC mutagenesis steps was used to introduce mutations into the ch36 sequence  
 CC to fully humanize the VH region (see ABR42719-31) and hence for the  
 CC production of an anti-human TF humanized antibody. Humanized antibodies  
 CC of the invention provide superior anticoagulant activity by binding  
 CC native human TF with high affinity and specificity. The antibodies bind  
 CC human TF, either alone or present in a TF:Factor VIIa complex,  
 CC effectively preventing Factor X (or Factor IX) binding to TF or the  
 CC complex, and thereby reducing blood coagulation. The humanized antibodies  
 CC are useful for inhibiting blood coagulation or blood clot formation,  
 CC angiogenesis, tumor metastases or inflammation in a mammal. They are  
 CC also useful as drug carriers, as cytotoxic agents, for reducing TF levels  
 CC in mammals, and for in vivo diagnosis  
 XX  
 XX Sequence 117 AA;  
 SQ  
 Query Match 94.7%; Score 584; DB 6; Length 117;  
 Best Local Similarity 93.2%; Pred. No. 4.4e-46;  
 Matches 109; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 ETLOQSGPELVKPGASVQVSKTGYSTFDNVVWVRSQSHKSLWIGYIDPYNGITY 60  
 DB 1 QILOQSGPELVKPGASVQVSKTGYSTFDNVVWVRSQSHKSLWIGYIDPYNGITY 60  
 QY 61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDSAVYFCARDVTTLDPFWGGTTLTVSS 117  
 DB 61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDSAVYFCARDVTTLDPFWGGTTLTVSS 117



XX Tissue factor; humanization; antibody; anticoagulant; cytostatic;  
 KW antiinflammatory; mouse; human.  
 XX Mus sp.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX Key Location/Qualifiers  
 FT Region 1..30 /note= "framework 1"  
 FT Misc-difference 1 /note= "wild-type Glu substituted by Gln"  
 FT Misc-difference 5 /note= "wild-type Val substituted by Gln"  
 FT Misc-difference 19 /note= "wild-type Gln substituted by Arg"  
 FT Misc-difference 24 /note= "wild-type Thr substituted by Ala"  
 FT Region 31..35 /note= "complementarity determining region 1"  
 FT Region 36..49 /note= "framework 2"  
 FT Misc-difference 41 /note= "wild-type His substituted by Pro"  
 FT Misc-difference 44 /note= "wild-type Ser substituted by Gly"  
 FT Region 50..66 /note= "complementarity determining region 2"  
 FT Region 67..98 /note= "framework 3"  
 FT Misc-difference 76 /note= "wild-type Ser substituted by Thr"  
 FT Misc-difference 77 /note= "wild-type Thr substituted by Ser"  
 FT Misc-difference 80 /note= "wild-type Phe substituted by Tyr"  
 FT Misc-difference 82 /note= "wild-type His substituted by Glu"  
 FT Misc-difference 84 /note= "wild-type Asn substituted by Ser"  
 FT Misc-difference 87 /note= "wild-type Thr substituted by Arg"  
 FT Misc-difference 89 /note= "wild-type Asp substituted by Glu"  
 FT Misc-difference 91 /note= "wild-type Ser substituted by Thr"  
 FT Region 99..106 /note= "complementarity determining region 3"  
 FT Region 107..117 /note= "framework 4"  
 FT Misc-difference 113 /note= "wild-type Leu substituted by Val"  
 FT WO2003037911-A2.  
 XX 08-MAY-2003.  
 XX 29-OCT-2002; 2002WO-US034727.  
 XX 29-OCT-2001; 2001US-0343306P.  
 XX 21-NOV-2001; 2001US-00990586.  
 XX (SUNO-) SUNOL MOLECULAR CORP.  
 XX Jiao J, Wong HC, Nieves EL, Mosquera LA;  
 XX WPI; 2003-468399/44.  
 XX New humanized antibody that binds specifically to human tissue factor,  
 PT useful for in vivo diagnostic methods, or for inhibiting blood  
 PT coagulation or blood clot formation, angiogenesis, tumor metastases or  
 PT inflammation in a mammal.

XX Claim 12; Fig 13; 110pp; English.  
 XX The present sequence is the protein sequence of a humanized version, HC-09, of the heavy chain variable region (VH) of anti-recombinant human tissue factor (TF) mouse-human chimeric antibody CH36. A series of PCR mutagenesis steps was used to introduce mutations into the CH36 sequence to fully humanize the VH region (see ABR42719-31) and hence for the production of an anti-human TF humanized antibody. Humanized antibodies of the invention provide superior anticoagulant activity by binding CC native human TF with high affinity and specificity. The antibodies bind CC human TF, either alone or present in a TF:Factor VIIa complex, CC effectively preventing Factor X (or Factor IX) binding to TF or the CC complex, and thereby reducing blood coagulation. The humanized antibodies CC are useful for inhibiting blood coagulation or blood clot formation, CC angiogenesis, tumour metastases or inflammation in a mammal. They are CC also useful as drug carriers, as cytotoxic agents, for reducing TF levels CC in mammals, and for in vivo diagnosis  
 XX Sequence 117 AA;  
 SQ Query Match 88.3%; Score 545; DB 6; Length 117;  
 Best Local Similarity 86.3%; Pred. No. 1.7e-42;  
 Matches 101; Conservative 9; Mismatches 7; Indels 0; Gaps 0;  
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 DB 1 QIQLVQSGPELVKPGASVRVSKASCYSFTDYNVYVWVROSPGKLEWIGYIDPYNGITYY 60  
 OY 61 DQNFKGKATLTVDKSTTAFMHLNLSLSDSDSAVYFCARDVTALDFFWGGTTLTVSS 117  
 DB 61 DQNFKGKATLTVDKSTTAFMHLNLSLSDSDSAVYFCARDVTALDFFWGGTTLTVSS 117  
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 ABR42731  
 ID ABR42731 standard; protein; 117 AA.  
 XX ABR42731;  
 XX 26-AUG-2003 (first entry)  
 XX Anti-tissue factor humanized antibody VH region HC-10.  
 XX Tissue factor; humanization; antibody; anticoagulant; cytostatic;  
 KW antiinflammatory; mouse; human.  
 XX Mus sp.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX Key Location/Qualifiers  
 FT Region 1..30 /note= "framework 1"  
 FT Misc-difference 1 /note= "wild-type Glu substituted by Gln"  
 FT Misc-difference 5 /note= "wild-type Val substituted by Gln"  
 FT Misc-difference 19 /note= "wild-type Gln substituted by Arg"  
 FT Misc-difference 24 /note= "wild-type Thr substituted by Ala"  
 FT Region 31..35 /note= "complementarity determining region 1"  
 FT Region 36..49 /note= "framework 2"  
 FT Misc-difference 41 /note= "wild-type His substituted by Pro"  
 FT Misc-difference 44 /note= "wild-type Ser substituted by Gly"  
 FT Region 50..66 /note= "complementarity determining region 2"  
 FT Region 67..98





PD 08-MAY-2003.  
XX  
PF 29-OCT-2002; 2002MO-US034727.  
XX  
XX 29-OCT-2001; 2001US-0343306P.  
PR 21-NOV-2001; 2001US-00990586.  
XX  
XX (SUNO-) SUNOL MOLECULAR CORP.  
PA  
XX Jiao J, Wong HC, Nieves EL, Mosquera LA;  
PI WPI; 2003-468399/44.  
XX  
XX New humanized antibody that binds specifically to human tissue factor,  
PT useful for in vivo diagnostic methods, or for inhibiting blood  
PT coagulation or blood clot formation, angiogenesis, tumor metastases or  
PT inflammation in a mammal.  
XX  
XX Claim 12; Fig 13; 110pp; English.  
XX  
CC The present sequence is the protein sequence of a humanized version, HC-  
CC 06, of the heavy chain variable region (VH) of anti-recombinant human  
CC tissue factor (TF) mouse-human chimeric antibody CH36. A series of PCR  
CC mutagenesis steps was used to introduce mutations into the CH36 sequence  
CC to fully humanize the VH region (see ABR42719-31) and hence for the  
CC production of an anti-human TF humanized antibody. Humanized antibodies  
CC of the invention provide superior anticoagulant activity by binding  
CC native human TF with high affinity and specificity. The antibodies bind  
CC human TF, either alone or present in a TF:Factor VIIa complex,  
CC effectively preventing Factor X (or Factor IX) binding to TF or the  
CC complex, and thereby reducing blood coagulation. The humanized antibodies  
CC are useful for inhibiting blood coagulation or blood clot formation,  
CC angiogenesis, tumour metastases or inflammation in a mammal. They are  
CC also useful as drug carriers, as cytotoxic agents, for reducing TF levels  
CC in mammals, and for in vivo diagnosis  
XX  
SQ Sequence 117 AA;  
  
Query Match 87.5%; Score 540; DB 6; Length 117;  
Best Local Similarity 85.5%; Pred. No. 5e-42;  
Matches 100; Conservative 10; Mismatches 7; Indels 0; Gaps 0;  
  
QY 1 EIQLOQSGELVKPGASVOVCKTGYSTDNVYVVRQSHGKSLWIGYIDPYNGITYY 60  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
1 QMLOQSGGELVKPGASVRVCKASGYSTDNVYVVRQSPGKLEWIGYIDPYNGITYY 60  
  
QY 61 DQNFKGKATLTVDKSTTAFMHLNLSLSDSAYVFCARDVTTLDFWGGGTTLTVSS 117  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
61 DQNFKGKATLTVDKSTTAFMHLNLSLSDSAYVFCARDVTTLDFWGGGTTLTVSS 117

Search completed: April 18, 2006, 13:35:38  
Job time : 190 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 18, 2006, 13:39:50 ; Search time 47 Seconds  
(without alignments)  
205.810 Million cell updates/sec

Title: US-10-764-140-4  
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Sequence: 1 ETQLQSGELVKPGASVQV.....RDVTALDFWQQTTLTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5-COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/6-COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H-COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS-COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE-COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfilea1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	616	99.8	117	1	US-08-814-806-4
2	616	99.8	117	2	US-09-293-854-4
3	521.5	84.5	118	2	US-09-847-468-139
4	521.5	84.5	118	2	US-09-847-468-140
5	521.5	84.5	137	2	US-09-647-468-153
6	521.5	84.5	137	2	US-09-647-468-154
7	484.5	78.5	116	1	US-08-273-146-55
8	478.5	77.6	118	2	US-09-647-468-144
9	478.5	77.6	137	2	US-09-647-468-158
10	473.5	76.7	116	1	US-08-672-345C-105
11	473.5	76.7	116	2	US-09-214-095D-90
12	473.5	76.7	116	2	US-09-940-727B-90
13	472	76.5	118	2	US-09-802-083-5
14	469.5	76.1	118	2	US-09-647-468-143
15	469.5	76.1	137	2	US-09-647-468-157
16	469	76.0	301	1	US-08-656-906-25
17	469	76.0	301	2	US-09-217-847-25
18	468.5	75.9	116	1	US-08-672-345C-106
19	467.5	75.8	116	1	US-07-634-278-56
20	467.5	75.8	116	1	US-08-477-728-56
21	467.5	75.8	116	1	US-08-474-040-56
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24	467.5	75.8	135	1	US-07-634-278-69
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28	467.5	75.8	135	1	US-08-137-117D-27	Sequence 27, Appl
29	467.5	75.8	135	1	US-08-436-717-27	Sequence 27, Appl
30	467.5	75.8	135	2	US-08-484-537-69	Sequence 69, Appl
31	465.5	75.4	116	1	US-08-672-345C-14	Sequence 14, Appl
32	465.5	75.4	116	2	US-09-214-095D-14	Sequence 14, Appl
33	465.5	75.4	116	2	US-09-940-727B-14	Sequence 14, Appl
34	462	74.9	132	2	US-08-434-000A-14	Sequence 14, Appl
35	462	74.9	132	2	US-09-312-157-14	Sequence 14, Appl
36	462	74.9	132	2	US-09-717-888-14	Sequence 14, Appl
37	454	73.6	130	2	US-09-556-605-3	Sequence 3, Appl
38	453.5	73.5	143	2	US-09-301-593-26	Sequence 26, Appl
39	453.5	73.5	472	2	US-09-301-593-30	Sequence 30, Appl
40	451	73.1	264	2	US-10-114-716A-46	Sequence 46, Appl
41	450	72.9	115	2	US-08-672-345C-16	Sequence 16, Appl
42	450	72.9	115	2	US-09-214-095D-16	Sequence 16, Appl
43	450	72.9	115	2	US-09-940-727B-16	Sequence 16, Appl
44	449.5	72.9	297	2	US-09-486-814A-2	Sequence 2, Appl
45	448.5	72.7	453	2	US-09-301-593-18	Sequence 18, Appl

## ALIGNMENTS

RESULT 1  
US-08-814-806-4  
; Sequence 4, Application US/08814806  
; Patent No. 5986065  
; GENERAL INFORMATION:  
; APPLICANT: Wong, Hing C.  
; APPLICANT: Jiao, Jin-an  
; APPLICANT: Esperanza, Nieves  
; APPLICANT: Lawrence, Luepschen  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD  
; TITLE OF INVENTION: COAGULATION AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/814,806  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Corless, Peter F  
; REGISTRATION NUMBER: 33,860  
; REFERENCE/DOCKET NUMBER: 46943  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 117 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:

US-08-814-806-4

Query Match 99.8%; Score 616; DB 1; Length 117;  
Best Local Similarity 100.0%; Pred. No. 2.9e-52; Mismatches 0; Indels 0; Gaps 0;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVVRQSHGKSLWIGYIDPYNGITIY 60  
Db 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVVRQSHGKSLWIGYIDPYNGITIY 60  
QY 61 DONFKGKATLTVDKSTTAFMHLNSLTSDSAVYFCARDVTTALDPWGQGTTLTVSS 117  
Db 61 DONFKGKATLTVDKSTTAFMHLNSLTSDSAVYFCARDVTTALDPWGQGTTLTVSS 117

RESULT 2

US-09-293-854-4  
; Sequence 4, Application US/09293854  
; Patent No. 6555319  
; GENERAL INFORMATION:  
; APPLICANT: Wong, Hing C.  
; Jiao, Jin-an  
; Esperanza, Nieves  
; Lawrence, Lupepschen  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD  
; COAGULATION AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Dike, Bronstein, Roberts & Cushman, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA: US/09/293,854  
APPLICATION NUMBER: US/09/293,854  
FILING DATE: 16-Apr-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/814,806  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Corleiss, Peter F  
REGISTRATION NUMBER: 33,860  
REFERENCE/DOCKET NUMBER: 46943  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-293-854-4

Query Match 99.8%; Score 616; DB 2; Length 117;  
Best Local Similarity 100.0%; Pred. No. 2.9e-52; Mismatches 0; Indels 0; Gaps 0;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVVRQSHGKSLWIGYIDPYNGITIY 60

Db 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVVRQSHGKSLWIGYIDPYNGITIY 60  
QY 61 DONFKGKATLTVDKSTTAFMHLNSLTSDSAVYFCARDVTTALDPWGQGTTLTVSS 117  
Db 61 DONFKGKATLTVDKSTTAFMHLNSLTSDSAVYFCARDVTTALDPWGQGTTLTVSS 117  
RESULT 3  
US-09-647-468-139  
; Sequence 139, Application US/09647468  
; Patent No. 6677436  
; GENERAL INFORMATION:  
; APPLICANT: SATO, KOH  
; APPLICANT: ADACHI, HIDEKI  
; APPLICANT: YABUTA, NAOHIRO  
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND  
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY  
; FILE REFERENCE: 053466/0289  
; CURRENT APPLICATION NUMBER: US/09/647,468  
; CURRENT FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: PCT/JP99/01768  
; PRIOR FILING DATE: 1999-04-02  
; PRIOR APPLICATION NUMBER: JP 10-91850  
; PRIOR FILING DATE: 1998-04-03  
; NUMBER OF SEQ ID NOS: 183  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 139  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Mus sp.  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF  
; OTHER INFORMATION: mouse monoclonal antibody ATR-2  
US-09-647-468-139

Query Match 84.5%; Score 521.5; DB 2; Length 118;  
Best Local Similarity 83.9%; Pred. No. 3.9e-43;  
Matches 99; Conservative 8; Mismatches 10; Indels 1; Gaps 1;  
QY 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVVRQSHGKSLWIGYIDPYNGITIY 60  
Db 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVVRQSHGKSLWIGYIDPYNGITIY 60  
QY 61 DONFKGKATLTVDKSTTAFMHLNSLTSDSAVYFCAR-DVTALDPWGQGTTLTVSS 117  
Db 61 NQFKGKATLTVDKSTTAFMHLNSLTSDSAVYFCARGGEGYFDYWGQGTTLTVSS 118

RESULT 4

US-09-647-468-140  
; Sequence 140, Application US/09647468  
; Patent No. 6677436  
; GENERAL INFORMATION:  
; APPLICANT: SATO, KOH  
; APPLICANT: ADACHI, HIDEKI  
; APPLICANT: YABUTA, NAOHIRO  
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND  
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY  
; FILE REFERENCE: 053466/0289  
; CURRENT APPLICATION NUMBER: US/09/647,468  
; CURRENT FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: PCT/JP99/01768  
; PRIOR FILING DATE: 1999-04-02  
; PRIOR APPLICATION NUMBER: JP 10-91850  
; PRIOR FILING DATE: 1998-04-03  
; NUMBER OF SEQ ID NOS: 183  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 140  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Mus sp.  
; FEATURE:

```

; OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-3
US-09-647-468-140

Query Match      84.5%; Score 521.5; DB 2; Length 118;
Best Local Similarity 83.9%; Pred. No. 3.9e-43;
Matches 99; Conservative 8; Mismatches 10; Indels 1; Gaps 1

Qy 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVYVWVQSHGKSLWIGYIDPYNGITTY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EIQLQSGPELVKPGASVKVSKASGYSFTDYNVYVWVQSHGKSLWIGYIDPYNGITTY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 DONPKGKATLTVDKSSSTAFMHLNSLTSDSVAVYFCAR-DVVTALDFWGGTTLTVSS 117
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFKGKATLTVDKSSSTAFMHLNSLTSDSVAVYFCARGEGYFDYWGQGTTLTVSS 118
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
US-09-647-468-153
; Sequence 153, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JF99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 153
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence coding for H chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-2
US-09-647-468-153

Query Match      84.5%; Score 521.5; DB 2; Length 137;
Best Local Similarity 83.9%; Pred. No. 4.6e-43;
Matches 99; Conservative 8; Mismatches 10; Indels 1; Gaps 1

Qy 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVYVWVQSHGKSLWIGYIDPYNGITTY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EIQLQSGPELVKPGASVKVSKASGYSFTDYNVYVWVQSHGKSLWIGYIDPYNGITTY 79
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 DONPKGKATLTVDKSSSTAFMHLNSLTSDSVAVYFCAR-DVVTALDFWGGTTLTVSS 117
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 NQKFKGKATLTVDKSSSTAFMHLNSLTSDSVAVYFCARGEGYFDYWGQGTTLTVSS 137
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
US-09-647-468-154
; Sequence 154, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JF99/01768

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```
; MOLECULE TYPE: protein
US-08-273-146-55

Query Match      78.5%; Score 484.5; DB 1; Length 116;
Best Local Similarity 76.1%; Pred. No. 1.4e-39;
Matches 89; Conservative 15; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVYVVRQSHGKSLWIGYIDPYNGITII 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLQSGPELVKPGASVKVSKASGYAFNINIVWVKQSHGKSLWIGYIDPYSGGSY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 DONFGKATLTVDKSSSTAFMHLNSLTSDSAVYFCARDVTYALD-FWGQGTTLTVSS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFKGKATLTVDKSSSTAFMHLNSLTSDSAVYFCAGG-NPRFAFWGQGTTLTVSS 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
US-09-647-468-144
; Sequence 144, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/J99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 144
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF mouse
; OTHER INFORMATION: monoclonal antibody ATR-8
US-09-647-468-144

Query Match      77.6%; Score 478.5; DB 2; Length 118;
Best Local Similarity 76.3%; Pred. No. 5.5e-39;
Matches 90; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVYVVRQSHGKSLWIGYIDPYNGITII 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQLQSGPELVKPGASVKVSKASGYSFTDYNIFWVKQSHGKSLWIGYIDPYTGTCY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 DONFGKATLTVDKSSSTAFMHLNSLTSDSAVYFCARDVTYALD-FWGQGTTLTVSS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFNDKATLTVDKSSSTAFMHLNSLTSDSAVYFCARGFYDYDCYWGQGTTLTVSA 118
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
US-09-647-468-158
; Sequence 158, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/J99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
```

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; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 158
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: sequence coding for H chain V region of anti-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-8
US-09-647-468-158

Query Match      77.6%; Score 478.5; DB 2; Length 137;
Best Local Similarity 76.3%; Pred. No. 6.5e-39;
Matches 90; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVYVVRQSHGKSLWIGYIDPYNGITII 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 DIQLQSGPELVKPGASVKVSKASGYSFTDYNIFWVKQSHGKSLWIGYIDPYTGTCY 79
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 DONFGKATLTVDKSSSTAFMHLNSLTSDSAVYFCARDVTYALD-FWGQGTTLTVSS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 NQKFNDKATLTVDKSSSTAFMHLNSLTSDSAVYFCARGFYDYDCYWGQGTTLTVSA 137
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
US-08-672-345C-105
; Sequence 105, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-672-345C-105

Query Match      76.7%; Score 473.5; DB 1; Length 116;
Best Local Similarity 75.2%; Pred. No. 1.6e-38;
Matches 88; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVYVVRQSHGKSLWIGYIDPYNGITII 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EIHLQSGPELVKPGASVKVSKASGYSFTDYNINWVKQSHGKSLWIGYIDPHNGGIFY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```







GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 18, 2006, 13:35:55 ; Search time 39 Seconds  
(without alignments)  
288.650 Million cell updates/sec

Title: US-10-764-140-4  
Perfect score: 617  
Sequence: 1 EIQLOQSGPELVKPGASVQV.....RDVTALDFWGGQTTLTVSS 117

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: Pir1.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	468.5	75.9	137	2 H32513	Ig heavy chain pre
2	465.5	75.4	139	2 A27609	Ig heavy chain pre
3	463	75.0	117	1 MHMS4E	Ig heavy chain v r
4	463	75.0	140	2 T01407	Ig heavy chain (my
5	461.5	74.8	128	2 I37267	Ig heavy chain v r
6	460	74.6	117	1 MHMSJ5	Ig heavy chain v r
7	452.5	73.3	119	2 F30502	Ig heavy chain v r
8	449	72.8	118	2 PL0200	anti-DNA autoantib
9	448.5	72.7	112	2 S09957	Ig heavy chain v-D
10	448	72.6	117	2 S03305	Ig heavy chain v r
11	446.5	72.4	120	2 A43982	Ig heavy chain v r
12	443	71.8	151	2 PL0011	Ig heavy chain pre
13	441.5	71.6	122	2 E37267	Ig heavy chain v r
14	441.5	71.6	128	2 C37267	Ig heavy chain v r
15	440	71.3	138	2 PH0105	anti-digoxin trans
16	439.5	71.2	135	2 PS0057	Ig heavy chain pre
17	438.5	71.1	114	2 S26319	Ig heavy chain v r
18	438	71.0	119	2 PH0099	Ig heavy chain v r
19	436	70.7	121	2 F37266	Ig heavy chain v r
20	435.5	70.6	469	2 S37483	Ig heavy chain v r
21	435.5	70.3	118	1 MHMS38	Ig gamma-2a chain
22	432	70.0	246	2 S38950	Ig heavy chain v r
23	432	70.0	446	2 S40295	Ig gamma chain - m
24	429.5	69.6	122	2 PH0887	Ig gamma-2a chain
25	429.5	69.6	128	2 A37267	Ig heavy chain v r
26	426.5	69.1	113	2 S55535	Ig heavy chain v r
27	426	69.0	166	2 PL0012	Ig heavy chain pre
28	425	68.9	121	2 H37266	Ig heavy chain v r
29	423.5	68.6	108	2 PH0975	Ig heavy chain v r

30	422	68.4	138	2 S45249	Ig heavy chain pre
31	421	68.2	117	2 S09961	Ig heavy chain v-D
32	421	68.2	119	2 B53285	Ig heavy chain v a
33	421	68.2	125	2 PH0100	Ig heavy chain v r
34	420.5	68.2	150	2 PN0444	Ig heavy chain v r
35	419.5	68.0	113	2 S55528	Ig heavy chain v r
36	419	67.9	116	2 S55542	Ig heavy chain v r
37	419	67.9	117	1 HVMS8A	Ig heavy chain v r
38	419	67.9	140	2 PH1482	Ig heavy chain pre
39	419	67.9	140	2 S04575	Ig heavy chain v r
40	418.5	67.8	131	2 S66537	Ig heavy chain pre
41	418	67.7	136	1 HVMSB1	Ig heavy chain v r
42	417.5	67.7	113	2 S55534	Ig heavy chain pre
43	417.5	67.7	117	2 S25176	Ig heavy chain v r
44	417.5	67.7	120	2 E45722	Ig heavy chain v r
45	417	67.6	113	2 PH0974	anti-glycoprotein
					Ig heavy chain v r

ALIGNMENTS

RESULT 1

H32513  
Ig heavy chain precursor V region (BXW16) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jan-2000  
C;Accession: H32513  
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;  
J. Clin. Invest. 82, 852-860, 1988  
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and  
A;Reference number: A94689; MUID:88331394; PMID:3138286  
A;Accession: H32513  
A;Molecule type: DNA  
A;Residues: 1-137 <KOF>  
A;Cross-references: UNIPARC:UPI0000114D9A; GB:M20831; NID:g196949; PIDN:AAA38848.1; PID  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match	75.9%;	Score	468.5;	DB	2;	Length	137;
Best Local Similarity	75.4%;	Pred. No.	1.3e-35;				
Matches	89;	Conservative	14;	Mismatches	14;	Indels	1;
Gaps	1;						
QY	1	EIQLOQSGPELVKPGASVQVCKTXGYSFTDYNVYVROSHGKSLWIGYIDPYNGITYY	60				
Db	20	EIQLOQSGAEVLKPGASVKISCKASGYSTGYNMVWKQSHGKSLWIGNINFYGSTSY	79				
QY	61	DNQFKGKATLTVDKSTTAFMHLNSLTSDSDSAVYFCAR-DVTALDFWGGQTTLTVSS	117				
Db	80	NQKFKGKATLTVDKSSSTAYMQLNSLTSDSDSAVYFCARKNYSGSFDYWGQTTLTVSS	137				

RESULT 2

A27609  
Ig heavy chain precursor V region (I29) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Dec-1988 #sequence\_revision 30-Jun-1991 #text\_change 23-Jul-1999  
C;Accession: A27609  
R;Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.  
J. Immunol. 140, 1676-1684, 1988  
A;Title: 1.29 lymphoma cells express a nonmutated V-H gene before and after H chain swi  
A;Reference number: A27609; MUID:88154467; PMID:3126234  
A;Accession: A27609  
A;Molecule type: DNA  
A;Residues: 1-139 <KLS>  
A;Cross-references: UNIPARC:UPI0000114D5D; EMBL:M19401; NID:g195441; PIDN:AAA38303.1; P  
C;Genetics:  
A;Introns: 16/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-139/Product: Ig heavy chain V region I29 #status predicted <VAR>  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 75.4%; Score 465.5; DB 2; Length 139;  
Best Local Similarity 72.5%; Pred. No. 2.4e-35;  
Matches 87; Conservative 18; Mismatches 12; Indels 3; Gaps 1;

QY 1 EIQLOQSGPELVKPGASVQVSKTXGYSTFDYNNVVRQSHGKSLWIGYIDPYNGITYIY 60  
DB 20 EVQLQOQSGPELVKPGASVQVSKTXGYSTFDYNNVVRQSHGKSLWIGYIDPYNDYTSY 79

QY 61 DONFKGKATLTVDKSSSTAFMHLNSLTSDSAVYFCAR---DVTALDFWGGGTTLTVSS 117  
DB 80 NQKFKGKATLTVDKSSSTAYMQLNSLTSDSAVYCYRYSYYSYAMDYWGOGTSVTVSS 139

RESULT 3  
MHMS4E  
Ig heavy chain V region (MOPC 104E) - mouse (tentative sequence)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Nov-1979 #sequence\_revision 14-Nov-1983 #text\_change 09-Jul-2004  
C:Accession: A02039  
R:Kehry, M.R.; Fuhrman, J.S.; Schilling, J.W.; Rogers, J.; Sibley, C.H.; Hood, L.E.  
Biochemistry 21, 5415-5424, 1982  
A:Title: Complete amino acid sequence of a mouse mu chain: homology among heavy chain co  
A:Reference number: A02039; MUID:83075344; PMID:6816276  
A:Accession: A02039  
A:Molecule type: protein  
A:Residues: 1-117 <KEH>  
A:Cross-references: UNIPROT:P01756; UNIPARC:UPI00000270F1  
C:Comment: The glycosylated asparagine residue does not have the usual N-X-S/T context a  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: glycoprotein; heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:22-96/Disulfide bonds: #status predicted  
F:55/Binding site: carbohydrate (Asn) (covalent) #status atypical

Query Match 75.0%; Score 463; DB 1; Length 117;  
Best Local Similarity 74.4%; Pred. No. 3.4e-35;  
Matches 87; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 EIQLOQSGPELVKPGASVQVSKTXGYSTFDYNNVVRQSHGKSLWIGYIDPYNGITYIY 60  
DB 1 EVQLQOQSGPELVKPGASVQVSKTXGYSTFDYNNVVRQSHGKSLWIGIDINPNNGGTSY 60

QY 61 DONFKGKATLTVDKSSSTAFMHLNSLTSDSAVYFCARDVTTALDFWGGGTTLTVSS 117  
DB 61 NQKFKGKATLTVDKSSSTAYMQLNSLTSDSAVYCARDYDFWVGNGITVTVSS 117

RESULT 4  
T01407  
Ig heavy chain (myeloma M104E) - mouse (fragment)  
C:Species: Mus sp. (mouse)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Jun-2000  
C:Accession: T01407  
R:Takahashi, S.; Matsura, Y.; Taniguchi, T.; Tamura, H.; Bitoh, S.; Onishi, S.; Yamamoto  
Microbiol. Immunol. 36, 855-863, 1992  
A:Title: Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic and  
A:Reference number: Z14317; MUID:9311638; PMID:1474935  
A:Accession: T01407  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-140 <TAK>  
A:Cross-references: UNIPARC:UPI000011B29E; EMBL:S51851; NID:9262657  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 75.0%; Score 463; DB 2; Length 140;  
Best Local Similarity 74.4%; Pred. No. 4.1e-35;  
Matches 87; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 EIQLOQSGPELVKPGASVQVSKTXGYSTFDYNNVVRQSHGKSLWIGYIDPYNGITYIY 60  
DB 20 EVQLQOQSGPELVKPGASVQVSKTXGYSTFDYNNVVRQSHGKSLWIGIDINPNNGGTSY 79

QY 61 DONFKGKATLTVDKSSSTAFMHLNSLTSDSAVYFCARDVTTALDFWGGGTTLTVSS 117  
DB 80 NQKFKGKATLTVDKSSSTAYMQLNSLTSDSAVYCARDYDFWVGNGITVTVSS 136

RESULT 5  
I37267  
Ig heavy chain V region (129) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 16-Aug-1996  
C:Accession: I37267  
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
J. Biol. Chem. 266, 6607-6613, 1991  
A:Title: Heavy and light chain variable region sequences and antibody properties of ant  
A:Reference number: A38740; MUID:91177923; PMID:1706720  
A:Accession: I37267  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-128 <RUF>  
A:Cross-references: UNIPARC:UPI0000176C52  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:19-102/Domain: immunoglobulin homology <IMM>

Query Match 74.8%; Score 461.5; DB 2; Length 128;  
Best Local Similarity 71.5%; Pred. No. 5.1e-35;  
Matches 88; Conservative 17; Mismatches 11; Indels 7; Gaps 2;

QY 2 IQLOQSGPELVKPGASVQVSKTXGYSTFDYNNVVRQSHGKSLWIGYIDPYNGITYIYD 61  
DB 6 VQLQOQSGPELVKPGASVQVSKTXGYSTFDYNNVVRQSHGKSLWIGIDINPNNGGTSY 65

QY 62 QNFYKATLTVDKSSSTAFMHLNSLTSDSAVYFCA-RDVTAL-----DFWGGGTTLT 114  
DB 66 QKFKGKATLTVDKSSSTAYMQLNSLTSDSAVYCARGLTTVAKSYDFWGGGTTLT 125

QY 115 VSS 117  
DB 126 VSS 128

RESULT 6  
MHMSJ5  
Ig heavy chain V region (J558) - mouse (tentative sequence)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 09-Jul-2004  
C:Accession: A26242  
R:Schilling, J.; Clevinger, B.; Davie, J.M.; Hood, L.  
Nature 283, 35-40, 1980  
A:Title: Amino acid sequence of homogeneous antibodies to dextran and DNA rearrangements  
A:Reference number: A26242; MUID:80078170; PMID:6765983  
A:Accession: A26242  
A:Molecule type: protein  
A:Residues: 1-117 <SCH>  
A:Cross-references: UNIPROT:P01757; UNIPARC:UPI00000270F2  
C:Note: the sequences of 10 hybridoma proteins that also bind dextran differ from that  
C:Comment: This protein binds dextran  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; hybridoma; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:22-96/Disulfide bonds: #status predicted

Query Match 74.6%; Score 460; DB 1; Length 117;  
Best Local Similarity 74.4%; Pred. No. 6.3e-35;  
Matches 87; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 EIQLOQSGPELVKPGASVQVSKTXGYSTFDYNNVVRQSHGKSLWIGYIDPYNGITYIY 60  
DB 1 EVQLQOQSGPELVKPGASVQVSKTXGYSTFDYNNVVRQSHGKSLWIGIDINPNNGGTSY 60

QY 61 DONFKGKATLTVDKSSSTAFMHLNSLTSDSAVYFCARDVTTALDFWGGGTTLTVSS 117  
DB 1 EVQLQOQSGPELVKPGASVQVSKTXGYSTFDYNNVVRQSHGKSLWIGIDINPNNGGTSY 60

```
Db 61 NQKFKGKATLTVDKSSSTAYMQLNSLTSDSAVYFCARDVYFDWVGAGTTTVSS 117

RESULT 7
Ig heavy chain V region (A52) - mouse
C:Species: Mus musculus (house mouse)
C:Accession: F30502
R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jatou, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies
A:Reference number: S09957
A:Accession: F30502
R:Ellat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice
A:Reference number: A30502; MUID:88315787; PMID:2457627
A:Accession: F30502
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <EIL>
A:Cross-references: UNIPARC:UPI0000176B33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.3%; Score 452.5; DB 2; Length 119;
Best Local Similarity 73.1%; Pred. No. 3.1e-34;
Matches 87; Conservative 12; Mismatches 17; Indels 3; Gaps 1;

QY 1 ETLOQSGPELVKPGASVQVSKTXGYSTFDYNNVYVWROSHGKSLWIGYIDPYNGITY 60
DB 1 ETLOQSGPELVKPGASVQVSKTXGYSTFDYNNVYVWROSHGKSLWIGYIDPYNGITY 60
QY 61 DQNFKGKATLTVDKSSSTAYMQLNSLTSDSAVYFCARDVYFDWVGAGTTTVSS 116
DB 61 NQKFKGKATLTVDKSSSTAYMQLNSLTSDSAVYFCARDVYFDWVGAGTTTVSS 119

RESULT 8
anti-DNA autoantibody BV16-19, heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: PL0200
R:Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A:Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from N
A:Reference number: PL0198; MUID:90309768; PMID:2114528
A:Accession: PL0200
A:Molecule type: mRNA
A:Residues: 1-118 <SMI>
A:Cross-references: UNIPARC:UPI0000113784; GB:X53641; NID:950193; PIDN:CAA37692.1; PID:9
F:15-98/Domain: immunoglobulin V region; immunoglobulin homology
F:31-35/Region: complementarity-determining 1
F:50-66/Region: complementarity-determining 2
F:99-110/Region: complementarity-determining 3
F:99-106/Region: D region
F:107-116/Region: JH region

Query Match 72.8%; Score 449; DB 2; Length 118;
Best Local Similarity 72.0%; Pred. No. 6.3e-34;
Matches 85; Conservative 14; Mismatches 15; Indels 4; Gaps 1;

QY 1 ETLOQSGPELVKPGASVQVSKTXGYSTFDYNNVYVWROSHGKSLWIGYIDPYNGITY 60
DB 1 ETLOQSGPELVKPGASVQVSKTXGYSTFDYNNVYVWROSHGKSLWIGYIDPYNGITY 60
QY 61 DQNFKGKATLTVDKSSSTAYMQLNSLTSDSAVYFCARDVYFDWVGAGTTTVSS 114
DB 61 NQKFKGKATLTVDKSSSTAYMQLNSLTSDSAVYFCARDVYFDWVGAGTTTVSS 118

RESULT 9
Ig heavy chain V-D-J region (106-10E) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Accession: S09957
R:Lin, C.; Kieber-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, T.
```

```
C:Species: Mus musculus (house mouse)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Jul-1999
C:Accession: S09957
R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jatou, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies
A:Reference number: S09955; MUID:90269328; PMID:2347362
A:Accession: S09957
A:Molecule type: mRNA
A:Residues: 1-112 <REI>
A:Cross-references: UNIPARC:UPI0000115E5C; EMBL:X51845; NID:955244; PIDN:CAA36138.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.7%; Score 448.5; DB 2; Length 112;
Best Local Similarity 72.6%; Pred. No. 6.7e-34;
Matches 85; Conservative 14; Mismatches 13; Indels 5; Gaps 1;

QY 1 ETLOQSGPELVKPGASVQVSKTXGYSTFDYNNVYVWROSHGKSLWIGYIDPYNGITY 60
DB 1 ETLOQSGPELVKPGASVQVSKTXGYSTFDYNNVYVWROSHGKSLWIGYIDPYNGITY 60
QY 61 DQNFKGKATLTVDKSSSTAYMQLNSLTSDSAVYFCARDVYFDWVGAGTTTVSS 117
DB 61 NQKFKGKATLTVDKSSSTAYMQLNSLTSDSAVYFCARDVYFDWVGAGTTTVSS 112

RESULT 10
Ig heavy chain V region (5B12) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C:Accession: JL0044; S05276; S03305
R:Van Cleave, V.H.; Naeve, C.W.; Metzger, D.W.
J. Exp. Med. 167, 1841-1848, 1988
A:Title: Do antibodies recognize amino acid side chains of protein antigens independent
A:Reference number: JL0043; MUID:88258372; PMID:2455014
A:Accession: JL0044
A:Molecule type: mRNA
A:Residues: 1-117 <VAN>
A:Cross-references: UNIPARC:UPI0000176B56; EMBL:X12381
R:Metzger, D.W.
submitted to the EMBL Data Library, July 1988
A:Reference number: S05276
A:Accession: S05276
A:Molecule type: mRNA
A:Residues: 1-116, 'T' <MET>
A:Cross-references: UNIPARC:UPI0000115DB3; EMBL:X12381; NID:952094; PIDN:CAA30939.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.6%; Score 448; DB 2; Length 117;
Best Local Similarity 72.6%; Pred. No. 7.7e-34;
Matches 85; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 1 ETLOQSGPELVKPGASVQVSKTXGYSTFDYNNVYVWROSHGKSLWIGYIDPYNGITY 60
DB 1 ETLOQSGPELVKPGASVQVSKTXGYSTFDYNNVYVWROSHGKSLWIGYIDPYNGITY 60
QY 61 DQNFKGKATLTVDKSSSTAYMQLNSLTSDSAVYFCARDVYFDWVGAGTTTVSS 117
DB 61 SQKFKGKATLTVDKSSSTAYMQLNSLTSDSAVYFCARDVYFDWVGAGTTTVSS 117

RESULT 11
Ig heavy chain V region (BA7.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: A49982
R:Lin, C.; Kieber-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, T.
```

```
J. Biol. Chem. 269, 2805-2813, 1994
A>Title: Topology of an amiloride-binding protein.
A|Reference number: A49982; MUID:94132051; PMID:8300613
A|Accession: A49982
A|Status: preliminary
A|Molecule type: mRNA
A|Residues: 1-120 <LIN>
A|Cross-references: UNIPARC:UPI0000114AA4; GB:L24802; NID:G452096; PIDN:AAA98740.1; PDB:
C|Superfamily: immunoglobulin V region; immunoglobulin homology
C|Keywords: heterotetramer; immunoglobulin
F|15-98/Domain: immunoglobulin homology <IMM>
```

	Query Match	72.4%	Score 446.5;	DB 2;	Length 120;
	Best Local Similarity	68.9%;	Pred. No. 1.1e-33;		
	Matches	84;	Conservative	18;	Mismatches 13;
				Indels	7;
				Gaps	2;
Qy	1	EIQLOQGPELVKPGASVOVSCKTXYGSFTDNYWYVQRSHGKSLEWMIGVIDPYNGITTY	60		
Dd	1	EVQLQQSGPELVKPGASVKISCKASGYSTFGYYIHMYKQSHSVKSLEWHIGHSPVNGATY	60		
Qy	61	DQNPKGRATILVDKSSSTAFMHNLNSLTDSDSAYVFCAI-----DVTTALDFWGOGTTLTV	115		
Dd	61	NQNFKDTASTILDKSSSTSYAWELHSLTSEDSAYVCARFNYYGHYT--MDYWGGGTSTVT	118		
Qy	116	SS 117			
Dd	119	SS 120			

C:Accession: E37267  
E:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
J. Biol. Chem. 266, 6607-6613, 1991  
A:Title: Heavy and light chain variable region sequences and antibody properties of anti-  
A:Reference number: A38740; MUID:91177923; PMID:1706720  
A:Accession: E37267  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-122 <RUF>  
A:Cross-references: UNIPARC:UPI0000176B3C  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:19-102/Domain: immunoglobulin homology <IMM>

Query Match 71.6%; Score 441.5; DB 2; Length 122;  
Best Local Similarity 69.7%; Pred. No. 3.1e-33;  
Matches 83; Conservative 20; Mismatches 11; Indels 5; Gaps 2;

Qy 2 IQLQSGPELVKPGASVQVSKTXGYSFTDYNVYRQSHGKSLIEWIGYIDPYNGITTYD 61  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 6 VQLQSGPELVKPGASVKISCKTGFYTFEYTHHWKQSHGKSLIEWIGGINPTGGTINN 65  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Qy 62 QNFKGGKATLTVDKSTTAFMHLNSLTSDSAVYFCFCA--PDVTALDFWGGGTTLTVSS 117  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 66 QKFRGKATLTVDKSSSTAYMELRLSTSDSAVYFCARRGREYT--MDYWGQGTSTVTS 122  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14  
C37267  
I9 heavy chain V region (Py69) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 21-Jan-2000  
C:Accession: C37267  
E:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
J. Biol. Chem. 266, 6607-6613, 1991  
A:Title: Heavy and light chain variable region sequences and antibody properties of anti-  
A:Reference number: A38740; MUID:91177923; PMID:1706720  
A:Accession: C37267  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-128 <RUF>  
A:Cross-references: UNIPARC:UPI0000176B3A  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:19-102/Domain: immunoglobulin homology <IMM>

Query Match 71.6%; Score 441.5; DB 2; Length 128;  
Best Local Similarity 66.7%; Pred. No. 3.3e-33;  
Matches 82; Conservative 19; Mismatches 15; Indels 7; Gaps 1;

Qy 2 IQLQSGPELVKPGASVQVSKTXGYSFTDYNVYRQSHGKSLIEWIGYIDPYNGITTYD 61  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 6 VQLQSGPELVKPGASVKISCKTGSYTFEYTHHWKQSHGKSLIEWIGRPNPNSGGSTYN 65  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Qy 62 QNFKGGKATLTVDKSTTAFMHLNSLTSDSAVYFCARD-----VTTALDFWGGGTTLT 114  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 66 QKFRGKATLTVDKSSSTAYMELRLSTSDSAVYFCARRGPGYGNVYTSYFDYWGQGTTLT 125  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Qy 115 VSS 117  
|||  
Db 126 VSS 128  
|||

RESULT 15  
PH0105  
anti-digoxin transfectoma antibody light chain V region precursor - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000  
C:Accession: PH0105  
E:Near, R.I.; Ng, S.C.; Mudgett-Hunter, M.; Hudson, N.W.; Margolies, M.N.; Seidman, J.G.  
Mol. Immunol. 27, 901-909, 1990  
A:Title: Heavy and light chain contributions to antigen binding in an anti-digoxin chain  
A:Reference number: PH0105; MUID:91015092; PMID:2120577

[illegible]

Search completed: April 18, 2006, 13:40:18  
Job time : 40 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 18, 2006, 13:40:31 ; Search time 165 Seconds  
(without alignments)  
296.279 Million cell updates/sec

Title: US-10-764-140-4  
Perfect score: 617  
Sequence: 1 ETQLQSGPELVKPGASVQV.....RDVTTALDFWGQGTTLTVSS 117

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.Main:\*  
1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	617	100.0	117	3	US-09-990-586-4
2	617	100.0	117	4	US-10-310-113-4
3	617	100.0	117	4	US-10-230-880-4
4	616	99.8	117	3	US-09-293-854-4
5	616	99.8	117	4	US-10-293-417-4
6	616	99.8	117	5	US-10-764-140-4
7	616	99.8	117	5	US-10-618-338-4
8	521.5	84.5	118	4	US-10-462-062-139
9	521.5	84.5	118	4	US-10-462-062-140
10	521.5	84.5	137	4	US-10-462-062-153
11	521.5	84.5	137	4	US-10-462-062-154
12	511.5	82.9	120	4	US-10-372-719-2
13	511.5	82.9	120	5	US-10-505-747-2
14	493	79.9	117	4	US-10-223-880-2
15	492	79.7	119	4	US-10-774-076-2
16	492	79.7	138	4	US-10-774-076-9
17	487	78.9	113	3	US-09-924-099-2
18	487	78.9	236	5	US-10-879-994-6
19	487	78.9	236	5	US-10-610-452-6
20	487	78.9	237	3	US-09-924-099-9
21	487	78.9	243	3	US-09-924-099-10
22	479.5	77.7	467	5	US-10-500-696-2
23	478.5	77.6	118	4	US-10-462-062-144
24	478.5	77.6	137	4	US-10-462-062-158
25	474.5	76.9	214	5	US-10-488-074-69
26	473.5	76.7	116	3	US-09-940-727B-90
27	472	76.5	118	3	US-09-802-083-5

28	472	76.5	118	4	US-10-165-732A-5
29	472	76.5	118	4	US-10-172-785-5
30	472	76.5	118	4	US-10-745-455-5
31	469.5	76.1	118	4	US-10-462-062-143
32	469.5	76.1	137	4	US-10-462-062-157
33	469.5	76.1	214	5	US-10-488-074-67
34	468.5	75.9	139	4	US-10-365-123-28
35	468.5	75.9	214	5	US-10-488-074-71
36	467.5	75.8	116	4	US-10-389-155-15
37	467.5	75.8	116	4	US-10-389-417-15
38	467.5	75.8	116	4	US-10-452-357-56
39	467.5	75.8	135	4	US-10-389-155-60
40	467.5	75.8	135	4	US-10-389-417-60
41	467.5	75.8	135	4	US-10-452-357-69
42	467.5	75.8	135	5	US-10-837-904-27
43	467.5	75.8	139	5	US-10-687-035-34
44	466	75.5	118	5	US-10-996-316-203
45	465.5	75.4	116	3	US-09-940-727B-14

ALIGNMENTS

RESULT 1  
US-09-990-586-4  
; Sequence 4, Application US/09990586  
; Publication No. US20030109680A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; APPLICANT: WONG, HING C.  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
; FILE REFERENCE: 71758/46943-CIP2  
; CURRENT APPLICATION NUMBER: US/09/990,586  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 117  
; TYPE: PPT  
; ORGANISM: Homo sapiens  
US-09-990-586-4

Query Match 100.0%; Score 617; DB 3; Length 117;  
Best Local Similarity 99.1%; Pred. No. 4.7e-52;  
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ETQLQSGPELVKPGASVQVSCRTQYSFTDYNVYVWVROSHGKSLWIGYIDPYNGITY 60  
Db 1 ETQLQSGPELVKPGASVQVSCRTQYSFTDYNVYVWVROSHGKSLWIGYIDPYNGITY 60  
QY 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDSVAVFCARDVTTLDFWGQGTTLTVSS 117  
Db 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDSVAVFCARDVTTLDFWGQGTTLTVSS 117

RESULT 2  
US-10-310-113-4  
; Sequence 4, Application US/10310113  
; Publication No. US20030176664A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; APPLICANT: WONG, HING C.  
; APPLICANT: NIEVES, ESPERANZA LILIANA  
; APPLICANT: MOSQUERA, LOUIS A.  
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING  
; FILE REFERENCE: 58122(71758)  
; CURRENT APPLICATION NUMBER: US/10/310,113  
; CURRENT FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 09/990,586

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; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Murine sp.
US-10-310-113-4

Query Match      100.0%; Score 617; DB 4; Length 117;
Best Local Similarity 99.1%; Pred. No. 4.7e-52;
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVYVWVROSHGKSLWIGYIDPYNGITIY 60
Db 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVYVWVROSHGKSLWIGYIDPYNGITIY 60

Qy 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGGTTLTVSS 117
Db 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGGTTLTVSS 117

RESULT 3
US-10-230-880-4
; Sequence 4, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-4

Query Match      100.0%; Score 617; DB 4; Length 117;
Best Local Similarity 99.1%; Pred. No. 4.7e-52;
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVYVWVROSHGKSLWIGYIDPYNGITIY 60
Db 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVYVWVROSHGKSLWIGYIDPYNGITIY 60

Qy 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGGTTLTVSS 117
Db 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGGTTLTVSS 117

RESULT 4
US-09-293-854-4
; Sequence 4, Application US/09293854
; Patent No. US20020168357A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Hing C.
```

```
; Jiao, Jin-an
; Esperanza, Nieves
; Lawrence, Lupeachen
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
; COAGULATION AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/293,854
; FILING DATE: 16-Apr-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/814,806
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Corless, Peter F.
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 46943
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-293-854-4

Query Match      99.8%; Score 616; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 5.9e-52;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVYVWVROSHGKSLWIGYIDPYNGITIY 60
Db 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVYVWVROSHGKSLWIGYIDPYNGITIY 60

Qy 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGGTTLTVSS 117
Db 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGGTTLTVSS 117

RESULT 5
US-10-293-417-4
; Sequence 4, Application US/10293417
; Publication No. US20030082636A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Hing C.
; Jiao, Jin-an
; Esperanza, Nieves
; Lawrence, Lupeachen
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
; COAGULATION AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
```



ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE  
COMPUTER: IBM COMPATIBLE  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ VERSION 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/293,417  
FILING DATE: 12-NOV-2003  
CLASSIFICATION: <UNKNOWN>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/293,854  
FILING DATE: 16-APR-1999  
APPLICATION NUMBER: 08/814,806  
FILING DATE: <UNKNOWN>  
ATTORNEY/AGENT INFORMATION:  
NAME: CORLESS, PETER F  
REGISTRATION NUMBER: 33,860  
REFERENCE/DOCKET NUMBER: 46943  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX: <UNKNOWN>  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-TERMINAL  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-293-417-4

Query Match 99.8%; Score 616; DB 4; Length 117;  
Best Local Similarity 100.0%; Pred. No. 5.9e-52;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EIQLQSGPELVKPGASVQVCKTGYSTFDYVWVROSHGKSLWIGYIDPYNGITY 60  
DB 1 EIQLQSGPELVKPGASVQVCKTGYSTFDYVWVROSHGKSLWIGYIDPYNGITY 60  
QY 61 DQNFKGKATLVKSTTAFMHLNSLTSDSAVYFCARDVTALDFWGGGTTLTSS 117  
DB 61 DQNFKGKATLVKSTTAFMHLNSLTSDSAVYFCARDVTALDFWGGGTTLTSS 117

RESULT 6  
US-10-764-140-4  
Sequence 4, Application US/10764140  
Publication No. US20040229282A1  
GENERAL INFORMATION:  
APPLICANT: WONG, HING C.  
APPLICANT: JIAO, JIN-AN  
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
TITLE OF INVENTION: OF USE THEREOF  
FILE REFERENCE: 59918 (71758)  
CURRENT APPLICATION NUMBER: US/10/764,140  
CURRENT FILING DATE: 2004-01-22  
PRIOR APPLICATION NUMBER: 10/293,417  
PRIOR FILING DATE: 2002-11-12  
PRIOR APPLICATION NUMBER: 09/293,854  
PRIOR FILING DATE: 2002-04-16  
PRIOR APPLICATION NUMBER: 08/814,806  
PRIOR FILING DATE: 2002-03-10

NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 4  
LENGTH: 117  
TYPE: PRT  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (25)  
OTHER INFORMATION: Variable amino acid  
US-10-764-140-4  
Query Match 99.8%; Score 616; DB 5; Length 117;  
Best Local Similarity 100.0%; Pred. No. 5.9e-52;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EIQLQSGPELVKPGASVQVCKTGYSTFDYVWVROSHGKSLWIGYIDPYNGITY 60  
DB 1 EIQLQSGPELVKPGASVQVCKTGYSTFDYVWVROSHGKSLWIGYIDPYNGITY 60  
QY 61 DQNFKGKATLVKSTTAFMHLNSLTSDSAVYFCARDVTALDFWGGGTTLTSS 117  
DB 61 DQNFKGKATLVKSTTAFMHLNSLTSDSAVYFCARDVTALDFWGGGTTLTSS 117  
RESULT 7  
US-10-618-338-4  
Sequence 4, Application US/10618338  
Publication No. US2005008929A1  
GENERAL INFORMATION:  
APPLICANT: WONG, HING C.  
JIAO, JIN-AN  
Esperanza, Nieves  
Lawrence, Luepschen  
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD  
COAGULATION AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE  
COMPUTER: IBM COMPATIBLE  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ VERSION 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/618,338  
FILING DATE: 11-JUL-2003  
CLASSIFICATION: <UNKNOWN>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/293,854  
FILING DATE: 16-APR-1999  
APPLICATION NUMBER: 08/814,806  
FILING DATE: <UNKNOWN>  
ATTORNEY/AGENT INFORMATION:  
NAME: CORLESS, PETER F  
REGISTRATION NUMBER: 33,860  
REFERENCE/DOCKET NUMBER: 46943  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX: <UNKNOWN>  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE

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;
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-618-338-4

Query Match          99.8%; Score 616; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 5.9e-52; Indels 0; Gaps 0;
Matches 117; Conservative 0; Mismatches 0;

QY 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVYVRQSHGKSLWIGYIDPYNGITIY 60
Db 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVYVRQSHGKSLWIGYIDPYNGITIY 60

QY 61 DONFKGKATLTVDKSSSTAFMHLNSLTSDSAVYFCARDVTTALDFWGGTTLTVSS 117
Db 61 DONFKGKATLTVDKSSSTAFMHLNSLTSDSAVYFCARDVTTALDFWGGTTLTVSS 117

RESULT 8
US-10-462-062-139
; Sequence 139, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
; TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
; FILE REFERENCE: 053466-0360
; CURRENT APPLICATION NUMBER: US/10/462,062
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence of
; OTHER INFORMATION: H chain V region of anti TF mouse monoclonal antibody ATR-2
US-10-462-062-139

Query Match          84.5%; Score 521.5; DB 4; Length 118;
Best Local Similarity 83.9%; Pred. No. 8.6e-43; Indels 1; Gaps 1;
Matches 99; Conservative 8; Mismatches 10;

QY 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVYVRQSHGKSLWIGYIDPYNGITIY 60
Db 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVYVRQSHGKSLWIGYIDPYNGITIY 60

QY 61 DONFKGKATLTVDKSSSTAFMHLNSLTSDSAVYFCAR-DVTTALDFWGGTTLTVSS 117
Db 61 DONFKGKATLTVDKSSSTAFMHLNSLTSDSAVYFCAR-DVTTALDFWGGTTLTVSS 117

RESULT 9
US-10-462-062-140
; Sequence 140, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
; TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
; FILE REFERENCE: 053466-0360
; CURRENT APPLICATION NUMBER: US/10/462,062
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 140
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
; OTHER INFORMATION: sequence for H chain V region of anti-TF mouse monoclonal
; OTHER INFORMATION: antibody ATR-2
US-10-462-062-140

Query Match          84.5%; Score 521.5; DB 4; Length 137;
Best Local Similarity 83.9%; Pred. No. 1e-42; Indels 1; Gaps 1;
Matches 99; Conservative 8; Mismatches 10;

QY 1 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVYVRQSHGKSLWIGYIDPYNGITIY 60
Db 20 EIQLQSGPELVKPGASVQVSKTXGYSFTDYNVYVRQSHGKSLWIGYIDPYNGITIY 79

QY 61 DONFKGKATLTVDKSSSTAFMHLNSLTSDSAVYFCAR-DVTTALDFWGGTTLTVSS 117
Db 80 NQKFKGKATLTVDKSSSTAFMHLNSLTSDSAVYFCAR-DVTTALDFWGGTTLTVSS 137

RESULT 11
US-10-462-062-154
; Sequence 154, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
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; APPLICANT: SATO, KOH  
; APPLICANT: ADACHI, HIDRKI  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)  
; FILE REFERENCE: 053466-0360  
; CURRENT APPLICATION NUMBER: US/10/462,062  
; CURRENT FILING DATE: 2003-06-16  
; PRIOR APPLICATION NUMBER: PCT/JP99/01768  
; PRIOR FILING DATE: 1999-04-02  
; PRIOR APPLICATION NUMBER: JP 10-91850  
; PRIOR FILING DATE: 1998-04-03  
; NUMBER OF SEQ ID NOS: 183  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 154  
; LENGTH: 137  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid  
; OTHER INFORMATION: sequence for H chain V region of anti-TF mouse monoclonal  
; OTHER INFORMATION: antibody ATTR-3  
US-10-462-062-154

Query Match 84.5%; Score 521.5; DB 4; Length 137;  
Best Local Similarity 83.9%; Pred. No. 1e-42; Indels 1; Gaps 1;  
Matches 99; Conservative 8; Mismatches 10; Indels 1; Gaps 1;  
QY 1 EIQLQSGPELVKPGASVQVSCCKTGYSTFDYNNVVRQSHGKSLWIGYIDPYNGITIY 60  
Db 20 EIQLQSGPELVKPGASVQVSCCKTGYSTFDYNNVVRQSHGKSLWIGYIDPYNGITIY 79  
QY 61 DONFKGKATLTVDKSTTAFMHLNSLTSDSAVYFCAR--DVTALDFWGGGTTLTVSS 117  
Db 80 NQKFGKATLTVDKSTTAFMHLNSLTSDSAVYFCAR--DVTALDFWGGGTTLTVSS 137

RESULT 12  
US-10-372-719-2  
; Sequence 2, Application US/10372719  
; Publication No. US20040005643A1  
; GENERAL INFORMATION:  
; APPLICANT: DE SANTIS, RITA  
; APPLICANT: ANASTASI, ANNA MARIA  
; TITLE OF INVENTION: ANTI-HUMAN TENASCIN MONOCLONAL ANTIBODY  
; FILE REFERENCE: 2818-141  
; CURRENT APPLICATION NUMBER: US/10/372,719  
; CURRENT FILING DATE: 2003-02-25  
; PRIOR APPLICATION NUMBER: 60/359,299  
; PRIOR FILING DATE: 2002-02-26  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: ST2146 heavy chain variable region protein sequence  
US-10-372-719-2

Query Match 82.9%; Score 511.5; DB 4; Length 120;  
Best Local Similarity 76.7%; Pred. No. 8.2e-42; Indels 3; Gaps 1;  
Matches 92; Conservative 17; Mismatches 8; Indels 3; Gaps 1;  
QY 1 EIQLQSGPELVKPGASVQVSCCKTGYSTFDYNNVVRQSHGKSLWIGYIDPYNGITIY 60  
Db 1 KVLQSGPELVKPGASVQVSCCKTGYSTFDYNNVVRQSHGKSLWIGYIDPYNGITIY 60  
QY 61 DONFKGKATLTVDKSTTAFMHLNSLTSDSAVYFCAR--DVTALDFWGGGTTLTVSS 117  
Db 61 NQKFGKATLTVDKSTTAFMHLNSLTSDSAVYFCAR--DVTALDFWGGGTTLTVSS 120

RESULT 13  
US-10-505-747-2  
; Sequence 2, Application US/10505747  
; Publication No. US20050106145A1  
; GENERAL INFORMATION:  
; APPLICANT: DE SANTIS, RITA  
; APPLICANT: ANASTASI, ANNA MARIA  
; TITLE OF INVENTION: ANTI-HUMAN TENASCIN MONOCLONAL ANTIBODY  
; FILE REFERENCE: 2818-141  
; CURRENT APPLICATION NUMBER: US/10/505,747  
; CURRENT FILING DATE: 2004-08-25  
; PRIOR APPLICATION NUMBER: 60/359,299  
; PRIOR FILING DATE: 2002-02-26  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: ST2146 heavy chain variable region protein sequence  
US-10-505-747-2

Query Match 82.9%; Score 511.5; DB 5; Length 120;  
Best Local Similarity 76.7%; Pred. No. 8.2e-42; Indels 3; Gaps 1;  
Matches 92; Conservative 17; Mismatches 8; Indels 3; Gaps 1;  
QY 1 EIQLQSGPELVKPGASVQVSCCKTGYSTFDYNNVVRQSHGKSLWIGYIDPYNGITIY 60  
Db 1 KVLQSGPELVKPGASVQVSCCKTGYSTFDYNNVVRQSHGKSLWIGYIDPYNGITIY 60  
QY 61 DONFKGKATLTVDKSTTAFMHLNSLTSDSAVYFCAR--DVTALDFWGGGTTLTVSS 117  
Db 61 NQKFGKATLTVDKSTTAFMHLNSLTSDSAVYFCAR--DVTALDFWGGGTTLTVSS 120

RESULT 14  
US-10-223-880-2  
; Sequence 2, Application US/10223880  
; Publication No. US20030152571A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON, KYUNG O.  
; APPLICANT: TAYLOR, ALEXANDER  
; TITLE OF INVENTION: ANIT-ALPHABETA3 HUMANIZED MONOCLONAL  
; TITLE OF INVENTION: ANTIBODIES  
; FILE REFERENCE: P50629C1  
; CURRENT APPLICATION NUMBER: US/10/223,880  
; CURRENT FILING DATE: 2002-08-20  
; PRIOR APPLICATION NUMBER: 09/380,910  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: PCT/US98/04987  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/039,609  
; PRIOR FILING DATE: 1997-03-12  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-223-880-2

Query Match 79.9%; Score 493; DB 4; Length 117;  
Best Local Similarity 76.1%; Pred. No. 4.9e-40; Indels 0; Gaps 0;  
Matches 89; Conservative 15; Mismatches 13; Indels 0; Gaps 0;  
QY 1 EIQLQSGPELVKPGASVQVSCCKTGYSTFDYNNVVRQSHGKSLWIGYIDPYNGITIY 60  
Db 1 KVLQSGPELVKPGASVQVSCCKTGYSTFDYNNVVRQSHGKSLWIGYIDPYNGITIY 60  
QY 61 DONFKGKATLTVDKSTTAFMHLNSLTSDSAVYFCAR--DVTALDFWGGGTTLTVSS 117





Strain	Sequence	Position
Qy	GAAGATTTGTAAATTATTACTGTCAACAAAGTTTACAGTTCTTCCATTACGTTCCGTTGCT	300
Db	GAAGATTTGTAAATTATTACTGTCAACAAAGTTTACAGTTCTTCCATTACGTTCCGTTGCT	300
Qy	GGGACCAAGCTGGAGCTGAAA	321
Db	GGGACCAAGCTGGAGCTGAAA	321

RESULT 2  
BD057834  
LOCUS  
BD057834 321 bp DNA linear PAT 27-AUG-2002  
DEFINITION  
Antibodies for inhibiting blood coagulation and methods of use thereof.

VERSION BD057834.1 GI:22603440  
KEYWORDS JP 2001516214-A/1.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE other sequences: artificial sequences.  
1 (bases 1 to 321)  
AUTHORS Wong,H.C.; Jiao,J.A.; Nieves,E.L. and Luespichen,L.  
TITLE Antibodies for inhibiting blood coagulation and methods of use  
JOURNAL Patent: JP 2001516214-A 1 25-SEP-2001;  
JP 2001516214-A 1

RESULT 3			
AR308506			
LOCUS	AR308506	321 bp	linear
		mrna	PAT 12-JUN-2003

DEFINITION	Sequence 1 from patent US 6555319.
ACCESSION	AR308506
VERSION	AR308506.1
KEYWORDS	GI:31699968
SOURCE	Unknown.
ORGANISM	Unknown.
	Unclassified.
REFERENCE	1 (bases 1 to 321)
AUTHORS	Wong,H.C., Jiao,J.-A., Nieves,E.L. and Luepschen,L.
TITLE	Antibodies for inhibiting blood coagulation and methods of use thereof
JOURNAL	Patent: US 6555319-A 1 29-APR-2003;
FEATURES	Sunol Molecular Corporation; Miramar, FL Location/Qualifiers

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RESULT 4
AR452626
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
AR452626
Sequence 12 from patent US 6677436.
AR452626
AR452626.1 GI:42684507
Unknown.
Unclassified.
1 (bases 1 to 375)
Sato,K., Adachi,H. and Yabuta,N.
Humanized antibody against human tissue factor (TF) and process of
production of the humanized antibody
Patent: US 6677436-A 12 13-JAN-2004;
Chugai Seiyaku Kabushiki Kaisha, Tokyo;
JPX;
Location/Qualifiers
1..375
/organism="unknown"
/mol type="genomic DNA"

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Db	55	GACATT	CAGATG	ACCAGT	CTCTG	CGCTCC	CCAGTCTG	CATCTCTG	GGGAAA	AGTGTCA	CC 114	
Qy	61	ATCACAT	GCGCTG	GCAAGT	CAGAC	CACTTG	ATGATAC	ATGTT	PAGCAT	TGGTAT	CAGCAGAAA	CCCA 120
Db	115	ATCACAT	GCGCTG	GCAAGT	CAGAC	CACTTG	ATGATAC	ATGTT	PAGCAT	TGGTAT	CAGCAGAAA	CCCA 174
Qy	121	GGGAAAT	CTCTC	TAGCT	CCTCAT	TATTAT	GCTG	CGCA	ACCAACTT	GGCAGAT	GGGGTCC	CAATCA 180
Db	175	GGGAAAT	CTCTC	TAGCT	CCTCAT	TATTAT	GCTG	CGCA	ACCAACTT	GGCAGAT	GGGGTCC	CAATCA 234
Qy	181	AGGTTT	CAGTGG	CAGTGG	ATCTG	GCACAAAA	TTTTCTTT	CTTCA	AGATC	CAGCAGCT	CAAGGCT	240
Db	235	AGGTTT	CAGTGG	TAGTGG	ATCTG	GCACAAAA	TTTTCTTT	CTTCA	AGATC	CAGCAGCT	CAAGGCT	294
Qy	241	GAAGAT	TTTTGT	ATAAT	TATTACT	GTGC	ACAA	CAAGT	TTTAC	AGTTCT	TCCATTC	ACCGTTCGGTGC 300
Db	295	GAAGAT	TTTTGT	ATAAT	TATTACT	GTGC	ACAA	CAAGT	TTTAC	AGTTCT	TCCATTC	ACCGTTCGGAGGG 354
Qy	301	GGGAC	CAAGCT	GGAGCT	GAAA							321
Db	355	GGGAC	CAAGCT	GGAAA	TAAAA							375

RESULT 5	AR452627	AR452627	Sequence 13 from patent US 6677436.	375 bp	DNA	linear	PAT 20-FEB-2004
LOCUS	AR452627	AR452627	GI:42684508				
DEFINITION	AR452627	AR452627					
ACCESSION	AR452627	AR452627					
VERSION	AR452627.1	AR452627.1					
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							

FEATURES	Location/Qualifiers
source	1..375
	/organism="unknown"
	/mol_type="genomic DNA"
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Query Match	91.5% Score 293.8; DB 6; Length 375;
Best Local Similarity	94.7%; pred.No. 2.2e-79;
Matches 304; Conservative	0; Mismatches 17; Indels 0; Gaps 0;

Qy	1	GACATT	CAGATG	ACCCAGT	CTCTCG	CCCTCC	CAGTCT	CGATCT	CTCGG	GAGAAAGT	GCACC	60
Db	55	GACATT	CAGATG	ACCCAGT	CTCTCG	CCCTCC	CAGTCT	CGATCT	CTCGG	GAGAAAGT	GCACC	114
Qy	61	ATC	CATG	CCCTG	GCAAGT	CA	GAC	CAAT	TGAT	ACAT	TGGTT	120
Db	115	ATC	ATG	CTG	CGC	AGT	CA	GAC	CAAT	TGGTT	AGCCT	174
Qy	121	GGG	AAAT	CTCT	C	T	C	A	G	T	C	180
Db	175	GGG	AAAT	CTCT	C	T	C	A	G	T	C	234
Qy	181	AGG	TT	C	A	G	T	C	A	G	T	240
Db	235	AGG	TT	C	A	G	T	C	A	G	T	294
Qy	241	GA	G	A	T	T	T	T	G	T	A	300
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Qy	301 GGGACCAAGCTGGAGCTGAAA	321
Dd		
	355 GGGACCAAGCTGGAAATAAAA	375
RESULT 6		
MMY13991		
LOCUS		
DEFINITION	Mus musculus mRNA for immunoglobulin VK domain of anti-viral haemorrhagic septicaemia virus, clone 3F1H10.	318 bp mRNA linear ROD 14-APR-2000
ACCESSION	Y13991	
VERSION	Y13991.1	GI:2222725
KEYWORDS	immunoglobulin; kappa chain; light chain; variable region.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;	
	Sciurognathi; Muridae; Murinae; Mus.	
	1 (bases 1 to 318)	
REFERENCE	Lorenzen,N., Olesen,N.J. and Jorgensen,P.E.	
AUTHORS	Neutralization of Egrevd virus pathogenicity to cell cultures and fish by monoclonal antibodies to the viral G protein	
TITLE	J. Gen. Virol. 71 (Pt 3), 561-567 (1990)	
JOURNAL		
PUBLISHED	1690259	
REFERENCE	2	

**JOURNAL** Lorenzen, N., Cupit, P.M., Secombes, C.J. and Cunningham, C.  
**PUBLISHED** Three monoclonal antibodies to the VHS virus glycoprotein:  
**TITLE** comparison of reactivity in relation to differences in  
immunoglobulin variable domain gene sequences  
**REFERENCE** Fish Shellfish Immunol. 10 (2), 129-142 (2000)  
10938729  
**AUTHORS** 3 (bases 1 to 318)  
**TITLE** Cupit, P.M.  
**JOURNAL** Direct Submission  
Submitted (24-JUN-1997) Cupit P.M., Molecular and Cell Biology,  
University of Aberdeen, Institute of Medical Science, Foresterhill,  
Aberdeen AB15 2YD SCOTLAND UK

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FEATURES             Location/Qualifiers
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                        /db_xref="taxon:10090"
                        /clone="3f1h10"
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                        /codon_start=1
                        /evidence=experimental
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	Best Local Similarity	95.0%;	Pred. No. 1.2e-78;		
	Matches 301;	Conservative 0;	Mismatches 16;	Indels 0;	Gaps 0;
Qy	1	GACATT	CAGATGACCCAGTCTCTGCGCTCCAGTCTGCATCTCTGGGAGAAAGTGTCA	CC	60
Db	1	GACATT	CAGATGACCCAGTCTCTGCGCTCCAGTCTGCATCTCTGGGAGAAAGTGTCA	CC	60
Qy	61	ATCACATGCTCG	CAAGTCAGACCACTTGATACATGGTTAGCATGTTATCAGCAGAAACCA		120
Db	61	ATCACATGCTCG	CAAGTCAGACCACTTGATACATGGTTAGCATGTTATCAGCAGAAACCA		120
Qy	121	GGGAAATCTCT	CAGTCTCTGATTTTATGCTGCCACCACTTGGCAGATGGGGTCCCATCA		180
Db	121	GGGAAATCTCT	CAGTCTCTGATTTTATGCTGCCACCACTTGGCAGATGGGGTCCCATCA		180

QY 181 AGGTTTCAGTGGAGTCTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240  
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 QY 301 GGGACCAAGCTGGAGCT 317  
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 Db 301 GGGACCAAGCTCGAGAT 317  
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RESULT 7  
 MMALCVR25 321 bp DNA linear ROD 31-AUG-1996  
 LOCUS M.musculus antibody light chain variable region (321bp).  
 DEFINITION X90900  
 ACCESSION  
 VERSION 2 (bases 1 to 321)  
 KEYWORDS antibody light chain; variable region.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE  
 1 Geiser, M. and Kretzschmar, T.

AUTHORS Unpublished  
 JOURNAL  
 REFERENCE 2 (bases 1 to 321)  
 AUTHORS Geiser, M.

TITLE Direct Submission  
 JOURNAL Submitted (17-AUG-1995) M. Geiser. CIBA-GEIGY LTD, CDDT,  
 K-681.5.46, CH-4002, Basel, SWITZERLAND

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## CDS

ORIGIN  
 Query Match 90.5%; Score 290.6; DB 9; Length 321;  
 Best Local Similarity 94.1%; Pred. No. 2.2e-78;  
 Matches 302; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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 Db 301 GGCACCAAGCTGGAATCAAA 321  
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## RESULT 8

MUSIGKADP 324 bp mRNA linear ROD 27-APR-1993  
 LOCUS Mouse Ig rearranged kappa-chain mRNA V-J region, partial cds.  
 DEFINITION M36760  
 ACCESSION  
 VERSION 1 GI:196619  
 KEYWORDS J-region; V-region; immunoglobulin light chain; processed gene.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE  
 1 (bases 1 to 324)  
 AUTHORS Clarke, S., Rickert, R., Wloch, M. K., Staudt, L., Gerhard, W. and Weigert, M.

TITLE The BALB/c secondary response to the Sb site of influenza virus hemagglutinin. Nonrandom silent mutation and unequal numbers of VH and Vk mutations  
 JOURNAL J. Immunol. 145 (7), 2286-2296 (1990)  
 PUBMED 2398280

COMMENT Original source text: Mouse (strain Balb/c), cDNA to mRNA, anti-influenza hemagglutinin hybridoma H37-92 Vk. Draft entry and computer-readable sequence for [J. Immunol. (1990) In press] kindly submitted by S. H. Clarke, 18-JUL-1990.

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 Chromosome 6.

ORIGIN  
 Query Match 90.2%; Score 289.4; DB 9; Length 324;  
 Best Local Similarity 93.1%; Pred. No. 5.1e-78;  
 Matches 299; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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QY 301 GGGACCAAGCTGGAGCTGAAA 321
Db 301 GGCACCAAGCTGGAAATCAAA 321

RESULT 9
MUSIGKADN
LOCUS 324 bp mRNA linear ROD 27-APR-1993
DEFINITION Mouse Ig rearranged kappa-chain mRNA V-J region, partial cds.
ACCESSION M36758
VERSION M36758.1 GI:196615
KEYWORDS J-region; V-region; immunoglobulin light chain; processed gene.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Clarke,S., Rickert,R., Wloch,M.K., Staudt,L., Gerhard,W. and Weigert,M.
TITLE The BALB/c secondary response to the Sb site of influenza virus hemagglutinin. Nonrandom silent mutation and unequal numbers of VH and VK mutations
JOURNAL J. Immunol. 145 (7), 2286-2296 (1990)
PUBMED 2398280
COMMENT Original source text: Mouse (strain Balb/c), cDNA to mRNA, anti-influenza hemagglutinin hybridoma H37-54 Vk. Draft entry and computer-readable sequence for [J. Immunol. (1990) In press] kindly submitted by S.H.Clarke, 18-JUL-1990.

FEATURES
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RLEIKR"
ORIGIN
Chromosome 6.

Query Match 90.0%; Score 288.8; DB 9; Length 324;
Best Local Similarity 93.1%; Pred. No. 7.9e-78;
Matches 299; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 GACATTCAGATGACCCAGTCTCTGCGTCCAGTCTGCAATCTCTGGGAGAAAGTGTCAACC 60
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QY 61 ATCACATGCTGGCAAGTCAGACCATTTGATACATGTTAGCATGGTATCAGCAGAAACCA 120
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QY 121 GGGAAATCTCTCAGCTCTGATTTATGCTGCACCAACTTTGGCAGATGGGTCCTCATCA 180
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QY 301 GGGACCAAGCTGGAGCTGAAA 321
Db 301 GGCACCAAGCTGGAAATCAAA 321

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RESULT 10
AX100597
LOCUS 1135 bp DNA linear PAT 10-APR-2001
DEFINITION Sequence 1 from Patent WO0121800.
ACCESSION AX100597
VERSION AX100597.1 GI:13619600
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE
AUTHORS Secombes,C.J., Cunningham,C. and Lorenzen,N.
TITLE Monoclonal antibody 3F1h10 neutralising vhsv (viral haemorrhagic septicaemia virus)
JOURNAL Patent: WO 0121800-A 1 29-MAR-2001;
ABERDEEN UNIVERSITY (GB) ; Statens Veterinaere Serumlaboratorium (DK)

FEATURES
source
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/mol_type="unassigned DNA"
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/notes="Description of Artificial Sequence:single chain antibody gene (BUI) inserted into E. coli pCDNA3 plasmid (Invitorgen)"
ORIGIN

Query Match 89.5%; Score 287.4; DB 6; Length 1135;
Best Local Similarity 93.5%; Pred. No. 1.9e-77;
Matches 300; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 GACATTCAGATGACCCAGTCTCTGCGTCCAGTCTGCAATCTCTGGGAGAAAGTGTCAACC 60
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QY 61 ATCACATGCTGGCAAGTCAGACCATTTGATACATGTTAGCATGGTATCAGCAGAAACCA 120
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QY 121 GGGAAATCTCTCAGCTCTGATTTATGCTGCACCAACTTTGGCAGATGGGTCCTCATCA 180
Db 598 GGGAAATCTCTCAGCTCTGATTTATGCTGCACCAACTTTGGCAGATGGGTCCTCATCA 657

QY 181 AGGTTCAAGTGGCAGTGTGATCTGCGCAAAAATTTCTTCAAGATCAGCAGCTTACAGGCT 240
Db 658 AGGTTCAAGTGTAGTGTGATCTGCGCAAAAATTTCTTCAAGATCAGCAGCTTACAGGCT 717

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Db 718 GAAGATTTTGTAAATTTACTGTCAACAACTTTACAGTACTCCGTACAGCTTCGGAGGG 777

QY 301 GGGACCAAGCTGGAGCTGAAA 321
Db 778 GGGACCAAGCTCGAGTCAAA 798

RESULT 11
AF302092
LOCUS 1135 bp DNA linear SYN 26-SEP-2002
DEFINITION Synthetic construct single chain antibody BUI gene, complete cds.
ACCESSION AF302092
VERSION AF302092.1 GI:11692742
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE
AUTHORS Lorenzen,N., Cupit,P.M., Einer-Jensen,K., Lorenzen,E., Ahrens,P., Secombes,C.J. and Cunningham,C.
TITLE Immunoprophylaxis in fish by injection of mouse antibody genes
JOURNAL Nat. Biotechnol. 18 (11), 1177-1180 (2000)
PUBMED 11062437

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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12: Geneseqn2004as.\*  
13: Geneseqn2004bs.\*  
14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	321	100.0	321	12	Adl35002 Murine an
3	321	100.0	321	13	Adu06807 Murine H3
4	321	100.0	321	14	Adw07325 Mouse ant
5	321	100.0	321	14	Adz40936 H36.D2.B7
6	310	96.6	322	9	Acc58568 Anti-tiss
7	293.8	91.5	375	2	Aaz33012 Anti-tiss
8	292.2	91.0	375	2	Aaz33013 Anti-tiss
9	289	90.0	949	14	Adz51613 High-func
10	287.4	89.5	1135	4	Aaf76338 Anti-VHSV
11	287	89.4	1300	2	Aat04179 C179Fv-Pp
12	285.8	89.0	949	14	Adz51605 High-func
13	285.4	88.9	1228	2	Aat04180 scFv-PP c
14	284.2	88.5	324	3	Aak99183 324nt DNA
15	282.6	88.0	949	14	Adz51609 High-func
16	281	87.5	949	14	Adz51611 High-func
17	281	87.5	949	14	Adz51615 High-func
18	279.4	87.0	949	14	Adz51607 High-func
19	278.4	86.7	312	2	Aaq41257 C23.5 VL

20	275.8	85.9	295	2	AAT04160	Aat04160 Anti-huma
21	239.4	74.6	321	3	Aaz88324	Aaz88324 Anti-zeta
22	239.4	74.6	366	2	AAD27166	Aad27166 Single ch
23	239.4	74.6	366	2	AAD27165	Aad27165 Single ch
24	239.4	74.6	366	4	AAD21541	Aad21541 Single ch
25	239.4	74.6	366	4	AAD21540	Aad21540 Single ch
26	239.4	74.6	366	6	ABSS3655	Abss3655 Anti-T-ce
27	239.4	74.6	366	6	ABSS3654	Abss3654 Anti-T-ce
28	239.4	74.6	366	12	ADJ88101	Adj88101 Wild type
29	239.4	74.6	366	12	ADJ88102	Adj88102 Single ch
30	239.4	74.6	366	13	ADR03283	Adr03283 DNA encod
31	239.4	74.6	366	13	ADR03284	Adr03284 DNA encod
32	239.4	74.6	367	2	AAx87211	Aax87211 scFv-KJ16
33	239.4	74.6	367	2	AAx87210	Aax87210 Wild-type
34	239.4	74.6	724	2	AAx90423	Aax90423 Chimeric
35	236.2	73.6	366	2	AAD27167	Aad27167 Single ch
36	236.2	73.6	366	4	AAD21542	Aad21542 Single ch
37	236.2	73.6	366	6	ABSS3656	Abss3656 Anti-T-ce
38	236.2	73.6	366	12	ADJ88103	Adj88103 Single ch
39	236.2	73.6	366	13	ADR03285	Adr03285 DNA encod
40	236.2	73.6	367	2	AAx87212	Aax87212 scFv-KJ16
41	236.2	73.6	1637	3	Aaz88358	Aaz88358 Bispecifi
42	233	72.6	1574	3	Aaz57599	Aaz57599 Erythrocy
43	231.4	72.1	324	3	AAx99634	Aax99634 Rat antib
44	231.4	72.1	324	10	ADB97811	Adb97811 HEV relat
45	231.4	72.1	384	2	AAT35973	Aat35973 Anti-huma

#### ALIGNMENTS

RESULT 1

AAV54961

ID AAV54961 standard; cDNA; 321 BP.

XX

AC AAV54961;

XX

DT 10-DEC-1998 (first entry)

XX

DE Human anti-tissue factor light chain variable region encoding cDNA.

XX

KW Human; anti-tissue factor light chain variable region; H36.D2.B7;

KW anti-tissue factor heavy chain variable region; inhibition; antibody;

KW blood coagulation; thrombosis; restenosis; thromboembolic condition;

KW cardiovascular; infection; neoplastic disease; clot; diagnosis; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

CDS 1..321

FT /\*tag= a

FT /product= "anti-tissue factor light chain variable

FT region"

FT /note= "no stop codon given"

FT

XX

PN WO9840408-A1.

XX

PD 17-SEP-1998.

XX

PP 10-MAR-1998; 98WO-US004644.

XX

PR 10-MAR-1997; 97US-00814806.

XX

PA (SUNO-) SUNOL MOLECULAR CORP.

XX

PI Wong HC, Jiao J, Nieves EL, Luepschen L;

XX

DR WPI; 1998-520804/44.

XX

PT New antibody to human tissue factor - used for, e.g. treating thrombosis

PT or restenosis or thromboembolic conditions associated with

PT cardiovascular, infectious or neoplastic disease.

XX Claim 11; Fig 1A; 53pp; English.  
PS The present sequence encodes the human anti-tissue factor light chain  
XX variable region from an antibody that binds native human tissue factor  
CC (TF) and does not bind non-native TF. The antibody capable of  
CC specifically binding native TF may be used for inhibiting blood  
CC coagulation and also for reducing TF levels in a mammal. The antibodies  
CC can be used, e.g. to treat thromboses, particularly to prevent or inhibit  
CC restenosis, or other thromboses following an invasive medical procedure  
CC such as arterial or cardiac surgery (e.g. angioplasty, endarterectomy,  
CC deployment of a stent, use of catheter, graft implantation or use of an  
CC arteriovenous shunt). The antibodies can also be used as a carrier for  
CC drugs, particularly pharmaceuticals targeted for interaction with a blood  
CC clot such as streptokinase, tissue plasminogen activator (t-PA) or  
CC urokinase, or a cytotoxic agent by conjugating a suitable toxin to the  
CC antibody. Further the antibodies can be used for treating a  
CC thromboembolic condition associated with cardiovascular disease, an  
CC infectious disease, a neoplastic disease or as a thrombolytic agent. The  
CC antibodies can also be used for detection and diagnosis  
XX  
SQ Sequence 321 BP; 85 A; 80 C; 73 G; 83 T; 0 U; 0 Other;

Query Match 100.0%; Score 321; DB 2; Length 321;  
Best Local Similarity 100.0%; Pred. No. 1.1e-92;  
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GACATTCAGATGACCCAGCTCTCTGCTCCAGTCTGCATCTCTGGAGAAAGTGTCCACC 60  
DB 1 GACATTCAGATGACCCAGCTCTCTGCTCCAGTCTGCATCTCTGGAGAAAGTGTCCACC 60  
QY 61 ATCATATGCTGGCAAGTCAGACCATTTGATATACATGTTAGCATGTTATCAGCAGAAACCA 120  
DB 61 ATCATATGCTGGCAAGTCAGACCATTTGATATACATGTTAGCATGTTATCAGCAGAAACCA 120  
QY 121 GGGAAATCTCTCAGCTCTGATTTATGTCGCCAACATTTGGCAGATGGGTGCCATCA 180  
DB 121 GGGAAATCTCTCAGCTCTGATTTATGTCGCCAACATTTGGCAGATGGGTGCCATCA 180  
QY 181 AGGTTTCAGTGGCAGTGGATCTGGCACAATAATTTCTTCAAGATCAGCAGCTACAGGCT 240  
DB 181 AGGTTTCAGTGGCAGTGGATCTGGCACAATAATTTCTTCAAGATCAGCAGCTACAGGCT 240  
QY 241 GAAGATTTTGTAAATTTACTGTCTCAACAAAGTTTACAGTTCTCCATTTCAGGTTCCGGTGT 300  
DB 241 GAAGATTTTGTAAATTTACTGTCTCAACAAAGTTTACAGTTCTCCATTTCAGGTTCCGGTGT 300  
QY 301 GGGACCAAGCTGGAGCTGAAA 321  
DB 301 GGGACCAAGCTGGAGCTGAAA 321

RESULT 2  
ADL35002  
ID ADL35002 standard; DNA; 321 BP.  
XX  
XX ADL35002;  
XX  
XX 03-JUN-2004 (first entry)  
XX  
XX Murine anti-tissue factor light chain antibody DNA SeqID 1.  
DE murine; mouse; humanised antibody; variable domain; framework region; FR;  
XX huFR; immune system molecule; H36.D2.B7; ss; gene; anti-tissue factor.  
XX  
XX Mus sp.  
XX  
XX Key Location/Qualifiers  
FH 1..321  
CDS /\*tag= a  
FT /partial  
FT /product= "H36.D2.B7 light chain protein"  
FT /note= "Start and stop codons are absent"  
FT

XX WO2004020579-A2.  
XX 11-MAR-2004.  
XX 06-AUG-2003; 2003WO-US024637.  
XX 29-AUG-2002; 2002US-00230880.  
XX (SUNO-) SUNOL MOLECULAR CORP.  
XX Wong HC, Stinson JR, Mosquera LA;  
PI WPI; 2004-239169/22.  
DR P-PSDB; ADL35003.  
PT Producing humanised antibodies for diagnostic and therapeutic purposes  
PT comprises optimizing similarity between individual antibody framework  
PT regions to help identify human framework regions suitable for making the  
PT antibodies.  
XX Disclosure; SEQ ID NO 1; 137pp; English.  
XX This invention relates to a novel method for producing a humanised  
CC antibody variable (V) domain or its fragment by optimising sequence  
CC similarity between individual antibody framework regions (FRs) in order  
CC to identify suitable human FRs (huFRs). Specifically, it refers to novel  
CC immune system molecules i.e. humanised monoclonal antibodies that exhibit  
CC suitable binding affinity with reduced immunogenicity in humans. The  
CC present invention describes a method of mutagenising DNA of non-human FRs  
CC to encode humanised FRs having an amino acid sequence that is  
CC substantially identical to the selected human FR previously identified  
CC through sequence similarity searching. As such, this method provides  
CC humanised light or heavy chain V domains of the sequence huFR1-huFR2  
CC -CDR2-huFR3-CDR3-huFR4, which can be used as therapeutic or diagnostic  
CC products to treat and/or diagnose diseases in humans and animals.  
CC Furthermore, the method expands the number of best fit possibilities that  
CC can be generated and provides a rational basis for assembling nearly all  
CC humanised immune system molecules of interest. This polynucleotide  
CC sequence is a murine anti-tissue factor light chain antibody H36.D2.B7  
CC DNA of the invention.  
XX  
SQ Sequence 321 BP; 85 A; 80 C; 73 G; 83 T; 0 U; 0 Other;  
Query Match 100.0%; Score 321; DB 12; Length 321;  
Best Local Similarity 100.0%; Pred. No. 1.1e-92;  
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCATCTCTGGAGAAAGTGTCCACC 60  
DB 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCATCTCTGGAGAAAGTGTCCACC 60  
QY 61 ATCATATGCTGGCAAGTCAGACCATTTGATATACATGTTAGCATGTTATCAGCAGAAACCA 120  
DB 61 ATCATATGCTGGCAAGTCAGACCATTTGATATACATGTTAGCATGTTATCAGCAGAAACCA 120  
QY 121 GGGAAATCTCTCAGCTCTGATTTATGTCGCCAACATTTGGCAGATGGGTGCCATCA 180  
DB 121 GGGAAATCTCTCAGCTCTGATTTATGTCGCCAACATTTGGCAGATGGGTGCCATCA 180  
QY 181 AGGTTTCAGTGGCAGTGGATCTGGCACAATAATTTCTTCAAGATCAGCAGCTACAGGCT 240  
DB 181 AGGTTTCAGTGGCAGTGGATCTGGCACAATAATTTCTTCAAGATCAGCAGCTACAGGCT 240  
QY 241 GAAGATTTTGTAAATTTACTGTCTCAACAAAGTTTACAGTTCTCCATTTCAGGTTCCGGTGT 300  
DB 241 GAAGATTTTGTAAATTTACTGTCTCAACAAAGTTTACAGTTCTCCATTTCAGGTTCCGGTGT 300  
QY 301 GGGACCAAGCTGGAGCTGAAA 321  
DB 301 GGGACCAAGCTGGAGCTGAAA 321

Query Match	100.0%	Score 321	DB 13	Length 321			
Best Local Similarity	100.0%	Pred. No. 1.le-92					
Matches 321	Conservative 0	Mismatches 0	Indels 0	Gaps 0			
Qy 1	GACATT	CAGATG	ACCCAGTCTCCTG	CTCCAGTCTGCATCTCTGGGAGAAAGTGTCA	CC 60		
Db 1	GACATT	CAGATG	ACCCAGTCTCCTG	CTCCAGTCTGCATCTCTGGGAGAAAGTGTCA	CC 60		
Qy 61	ATCACATG	CCCTG	CGCAAGTCAGACCA	TGATGATCATGGTTAGCATGGTATCAGCAGAAACCA	120		
Db 61	ATCACATG	CCCTG	CGCAAGTCAGACCA	TGATGATCATGGTTAGCATGGTATCAGCAGAAACCA	120		
Qy 121	GGGAAATCTCT	CAGCTCT	CCTGATTTATGCTGCCACCA	AACTTTGGCAGATGGGGTCCCATCA	180		
Db 121	GGGAAATCTCT	CAGCTCT	CCTGATTTATGCTGCCACCA	AACTTTGGCAGATGGGGTCCCATCA	180		
Qy 181	AGGTTTCAGTGG	CAGTGGATCTGG	CACAAAATTTCTTTCAAGATCAGACGCTACAGGCT	240			
Db 181	AGGTTTCAGTGG	CAGTGGATCTGG	CACAAAATTTCTTTCAAGATCAGACGCTACAGGCT	240			
Qy 241	GAAGATTTTGTAA	ATTATTA	CTGTCACACAGTTTACAGTTCTTCCATTCACGTTCCGGT	300			
Db 241	GAAGATTTTGTAA	ATTATTA	CTGTCACACAGTTTACAGTTCTTCCATTCACGTTCCGGT	300			
Qy 301	GGGACCAAGCT	GGAGCTG	AA 321				
Db 301	GGGACCAAGCT	GGAGCTG	AA 321				
RESULT 4							
ADW07325							
ID	ADW07325 standard; cDNA; 321 BP.						
AC	ADW07325;						
DT	07-APR-2005 (first entry)						
DE	Mouse anti-tissue factor antibody H36.D2.B7 VL cDNA.						
KW	Blood-clotting; light chain variable region; inflammation;						
KW	antiinflammatory; antibody; ss; tissue factor; sepsis;						
KW	disseminated intravascular coagulation; anticoagulant;						
KW	hematological disease; thrombosis; lung injury; respiratory-gen.;						
KW	respiratory distress syndrome; immunosuppressive; Antibacterial;						
KW	Antiarthritic; Antianemic; anemia; rheumatoid arthritis;						
KW	glomerulonephritis; multiple sclerosis; psoriasis; Sjogren's syndrome;						
KW	inflammatory bowel disease.						
OS	Mus sp.						
FH	Key Location/Qualifiers						
FT	CDS	1..321					
FT	FT	/*tag= a					
FT	FT	/product= "Light chain"					
FT	FT	/partial					
FT	FT	/note= "No start or stop codon shown"					
XX	WO2005004793-A2.						
XX	20-JAN-2005.						
XX	04-JUN-2004; 2004WO-US017900.						
XX	19-JUN-2003; 2003US-0480254P.						
XX	22-JAN-2004; 2004US-0538892P.						
XX	(SUNO-) SUNOL MOLECULAR CORP.						
XX	Jiao J, Wong HC, Egan JO;						
XX	WPI; 2005-091964/10.						
DR	P-PSDB; ADW07326.						

XX	Preventing or treating sepsis or inflammation in mammals comprises administering a humanized or chimeric antibody that binds to a human tissue factor to form a complex in which factor X or IX binding to the complex is inhibited.	
PS	Disclosure, SEQ ID NO 1; 109pp; English.	
XX		
CC	The invention relates to preventing or treating a sepsis or inflammatory disease in a mammal comprising administering to the mammal a therapeutic amount of at least one humanized antibody, chimeric antibody, or their fragment that binds specifically to tissue factor (TF) to form a complex, where factor X or IX binding to the complex is inhibited and the administration prevents or treats the sepsis in the mammal. Also included are a kit for performing the above method and reducing an inflammatory cytokine production in a mammal. The inflammatory disease is associated with arthritis (preferably rheumatoid arthritis), glomerulonephritis, multiple sclerosis, psoriasis, Sjogren's syndrome, or inflammatory bowel disease. The method also treats or prevents a sepsis-induced anemia or a sepsis-related condition in a mammal, where the sepsis-related condition is DIC, fibrin deposition, thrombosis, lung injury, or sepsis-associated renal disorder. The lung injury is acute lung injury (ALI) or acute respiratory distress syndrome (ARDS). The sepsis-associated renal disorder is acute tubular necrosis. The methods and kit are useful for preventing or treating sepsis or sepsis-related conditions (e.g. DIC or anemia) or inflammatory diseases (e.g. arthritis). The humanized antibodies are based on the chimeric antibody CH36 which comprises the light and heavy chain variable regions (VL or VH) of an anti-TF antibody fused to the human IgG4 heavy and kappa light constant regions. The CDRs (complementarity determining region) and F&E (framework regions) are then humanized. The present sequence encodes the light or heavy chain variable region of the anti-TF antibody (wild-type).	
XX		
SQ	Sequence 321 BP; 85 A; 80 C; 73 G; 83 T; 0 U; 0 Other;	
	Query Match 100.0%; Score 321; DB 14; Length 321;	
	Best Local Similarity 100.0%; Pred. No. 1.1e-92;	
	Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 GACATTCAGATGACCCAGTCTCCCTGCCCTCCAGCTGCATCTCTGGGAGAAAGTGTCA	60
Db	1 GACATTCAGATGACCCAGTCTCCCTGCCCTCCAGCTGCATCTCTGGGAGAAAGTGTCA	60
Qy	61 ATCATATGCTCCGCAAGTCAGACCATTCATATCATGTTAGCATGGTATCAGCAGAAACCA	120
Db	61 ATCATATGCTCCGCAAGTCAGACCATTCATATCATGTTAGCATGGTATCAGCAGAAACCA	120
Qy	121 GGGAAATCTCTCAGTCTCTGATTTATGCTGCCACCAACTTGGCGAGATGGGGTCCCATCA	180
Db	121 GGGAAATCTCTCAGTCTCTGATTTATGCTGCCACCAACTTGGCGAGATGGGGTCCCATCA	180
Qy	181 AGGTTTCAGTGGCAGTGGATCTGGCACAATAATTTCTTTTCAGATCAGCAGCTACAGCT	240
Db	181 AGGTTTCAGTGGCAGTGGATCTGGCACAATAATTTCTTTTCAGATCAGCAGCTACAGCT	240
Qy	241 GAAGATTTTGTAAATTTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTTCGGTGTCT	300
Db	241 GAAGATTTTGTAAATTTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTTCGGTGTCT	300
Qy	301 GGGACCAAGCTGGAGCTGAAA 321	
Db	301 GGGACCAAGCTGGAGCTGAAA 321	
RESULT 5		
AD240936		
ID	AD240936 standard; DNA; 321 BP.	
XX		
AC	AD240936;	
XX		
DT	14-JUL-2005 (first entry)	
XX		
DE	H36.D2.B7 anti-tissue factor light chain variable region encoding DNA.	



```

QY 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCATCTCTGGGAGAAAGTGTCAAC 60
Db 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCATCTCTGGGAGAAAGTGTCAAC 60
QY 61 ATCAGATGCTGGCAAGTCAGACCAATGATACATGTTAGCATGGTATCAGCAGAAACCA 120
Db 61 ATCAGATGCTGGCAAGTCAGACCAATGATACATGTTAGCATGGTATCAGCAGAAACCA 120
QY 121 GGGAAATCTCTCAGCTCTGATTTATGCTGCCACCAACTTGGCAGATGGGTGCCATCA 180
Db 121 GGGAAATCTCTCAGCTCTGATTTATGCTGCCACCAACTTGGCAGATGGGTGCCATCA 180
QY 181 AGTTTCAGTGGCAGTGGATCTGGCAGCAAAATTTTCTTCAAGATCAGCAGCCTACAGGCT 240
Db 181 AGTTTCAGTGGCAGTGGATCTGGCAGCAAAATTTTCTTCAAGATCAGCAGCCTACAGGCT 240
QY 241 GAAGATTTTGTAAATTTACTGTCAACAGTTTACAGTTCTCCATTCAGTTTCGGTGCT 300
Db 241 GAAGATTTTGTAAATTTACTGTCAACAGTTTACAGTTCTCCATTCAGTTTCGGTGCT 300
QY 301 GGGACCAAGCTGGAGCTGAAA 321
Db 301 GGGACCAAGCTGGAGCTGAAA 321

RESULT 6
ACC58568
ID ACC58568 standard; cDNA; 322 BP.
XX
AC ACC58568;
XX
DT 26-AUG-2003 (first entry)
XX
DE Anti-tissue factor antibody H36.D2.B7 VL coding sequence.
XX
KW Tissue factor; antibody; H36.D2.B7; anticoagulant; cytostatic;
KW antiinflammatory; mouse; gene; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
CDS 1..322
FT /tag= a
FT /partial
FT /product= "H36.D2.B7 VL"
FT /transl_except= (pos:256..259,aa:Tyr)
FT /note= "this codon has an apparent 1 nucleotide insertion
FT which alters the reading frame; the CDS has no start or
FT stop codon"
XX
PN WO2003037911-A2.
XX
PD 08-MAY-2003.
XX
PF 29-OCT-2002; 2002WO-US034727.
XX
PR 29-OCT-2001; 2001US-0343306P.
PR 21-NOV-2001; 2001US-00990586.
XX
PA (SUNO-) SUNOL MOLECULAR CORP.
XX
PI Jiao J, Wong HC, Nieves EL, Mosquera LA;
XX
DR WPI; 2003-468399/44.
DR P-PSDB; ABR42699.
XX
PT New humanized antibody that binds specifically to human tissue factor,
PT useful for in vivo diagnostic methods, or for inhibiting blood
PT coagulation or blood clot formation, angiogenesis, tumor metastases or
PT inflammation in a mammal.
XX
PS Example 1; Fig 1A; 110pp; English.

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CC The present sequence is the coding sequence for the light chain variable
CC region (VL) of anti-recombinant human tissue factor (TF) murine antibody
CC H36.D2.B7 (ATCC HB-12255). The invention relates to antibodies,
CC especially humanized H36.D2.B7, that provide superior anticoagulant
CC activity by binding native human TF with high affinity and specificity.
CC The antibodies bind human TF, either alone or present in a TF:Factor VIIa
CC complex, effectively preventing Factor X (or Factor IX) binding to TF or
CC the complex, and thereby reducing blood coagulation. The humanized
CC antibodies are useful for inhibiting blood coagulation or blood clot
CC formation, angiogenesis, tumor metastases or inflammation in a mammal.
CC They are also useful as drug carriers, as cytotoxic agents, for reducing
CC TF levels in mammals, and for in vivo diagnosis
XX
SQ Sequence 322 BP; 85 A; 80 C; 73 G; 84 T; 0 U; 0 Other;
Query Match 96.6%; Score 310; DB 9; Length 322;
Best Local Similarity 99.7%; Pred. No. 3.8e-89;
Matches 321; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCATCTCTGGGAGAAAGTGTCAAC 60
Db 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCATCTCTGGGAGAAAGTGTCAAC 60
QY 61 ATCAGATGCTGGCAGTGGATCTGGCAGCAAAATTTTCTTCAAGATCAGCAGCCTACAGGCT 120
Db 61 ATCAGATGCTGGCAGTGGATCTGGCAGCAAAATTTTCTTCAAGATCAGCAGCCTACAGGCT 120
QY 121 GGGAAATCTCTCAGCTCTGATTTATGCTGCCACCAACTTGGCAGATGGGTGCCATCA 180
Db 121 GGGAAATCTCTCAGCTCTGATTTATGCTGCCACCAACTTGGCAGATGGGTGCCATCA 180
QY 181 AGTTTCAGTGGCAGTGGATCTGGCAGCAAAATTTTCTTCAAGATCAGCAGCCTACAGGCT 240
Db 181 AGTTTCAGTGGCAGTGGATCTGGCAGCAAAATTTTCTTCAAGATCAGCAGCCTACAGGCT 240
QY 241 GAAGATTTTGTAAATTTACTGTCAACAGTTTACAGTTCTCCATTCAGTTTCGGTGCT 299
Db 241 GAAGATTTTGTAAATTTACTGTCAACAGTTTACAGTTCTCCATTCAGTTTCGGTGCT 300
QY 300 TGGGACCAAGCTGGAGCTGAAA 321
Db 301 TGGGACCAAGCTGGAGCTGAAA 322

RESULT 7
AAZ33012
ID AAZ33012 standard; DNA; 375 BP.
XX
AC AAZ33012;
XX
DT 26-JAN-2000 (first entry)
XX
DE Anti-tissue factor mouse monoclonal antibody ATR-2 L chain V region DNA.
XX
KW Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
KW ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
KW disseminated intravascular coagulation; immunogenicity; chimeric; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN WO9951743-A1.
XX
PD 14-OCT-1999.
XX
PF 02-APR-1999; 99WO-JP001768.
XX
PR 03-APR-1998; 98JP-00091850.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Sato K, Adachi H, Yabuta N;
XX

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DR WPI; 1999-620204/53.  
 XX P-PSDB; AAY52761.  
 XX Humanised antibody recognizing human tissue factor, used for treatment of  
 PT disseminated intravascular coagulation.  
 XX  
 XX Example 1; Page 190-191; 291pp; Japanese.  
 XX  
 CC The present invention describes chimeric antibody (Ab) heavy (H) chains  
 CC containing the variable region of the H chain of a mouse monoclonal Ab  
 CC recognising human tissue factor (hTF) and the constant region of the H  
 CC chain of a human Ab. The variable region is one of six specified  
 CC sequences (which are the H chain variable regions from mouse monoclonal  
 CC Ab's ATR-2, 3, 4, 5, 7 or 8). Also described are chimeric Ab light (L) chains  
 CC containing the variable region of the L chain of a mouse monoclonal Ab  
 CC recognising human tissue factor (hTF) and the constant region of the L  
 CC chain of a human Ab, the variable region being one of six specified  
 CC sequences (which are the L chain variable regions from mouse monoclonal  
 CC Ab's ATR-2, 3, 4, 5, 7 or 8). The chimeric Ab's can be used for the treatment  
 CC and prevention of thrombotic disease, especially of disseminated  
 CC intravascular coagulation (DIC). The humanised antibody has the high hTF  
 CC binding activity of the mouse monoclonal antibody but greatly reduced  
 CC immunogenicity. AAZ33001 to AAZ33091 and Y527007 to AAY52767 represent  
 CC sequences used in the exemplification of the present invention  
 XX  
 SQ Sequence 375 BP; 96 A; 89 C; 92 G; 98 T; 0 U; 0 Other;  
 Query Match 91.5%; Score 293.8; DB 2; Length 375;  
 Best Local Similarity 94.7%; Pred. No. 6.5e-84;  
 Matches 304; Conservative 0; Mismatches 17; Indels 0; Gaps 0;  
 QY 1 GACATTGAGTACAGCCAGTCTCTGCTCCAGTCTGCATCTCTGGGAGAAAGTGTACCC 60  
 DB 55 GACATTGAGTACAGCCAGTCTCTGCTCCAGTCTGCATCTCTGGGAGAAAGTGTACCC 114  
 QY 61 ATCACATGCTGGCAAGTCAGACCATTTGATATACATGTTAGCATGGTATCAGCAGAAACCA 120  
 DB 115 ATCACATGCTGGCAAGTCAGACCATTTGATATACATGTTAGCATGGTATCAGCAGAAACCA 174  
 QY 121 GGGAAATCTCTCAGTCTGATTTATGCTGCCACCACTTGGCAGATGGGTCCCATCA 180  
 DB 175 GGGAAATCTCTCAGTCTGATTTATGCTGCCACCACTTGGCAGATGGGTCCCATCA 234  
 QY 181 AGGTTTCAGTGGCAGTGGATCTGGCACAATAATTTCTTTCAAGATCAGCAGCTACAGGCT 240  
 DB 235 AGGTTTCAGTGGTGGATCTGGCACAATAATTTCTTTCAAGATCAGCAGCTACAGGCT 294  
 QY 241 GAAGATTTGTAAATTTACTGTCAACAAAGTTTACAGTTCTCCATTCAGTTTCGGTGTCT 300  
 DB 295 GAAGATTTGTAAATTTACTGTCAACAACTTTACAGTACTCCGTACACGTTTCGGAGGG 354  
 QY 301 GGGACCAAGCTGGAGCTGAAA 321  
 DB 355 GGGACCAAGCTGGAAATAAAA 375  
 RESULT 8  
 ID AAZ33013 standard; DNA; 375 BP.  
 XX AAZ33013;  
 XX AAZ33013;  
 DT 26-JAN-2000 (first entry)  
 XX  
 DE Anti-tissue factor mouse monoclonal antibody ATR-3 L chain V region DNA.  
 XX  
 KW Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;  
 KW ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;  
 KW disseminated intravascular coagulation; immunogenicity; chimeric; aa.  
 XX  
 OS Synthetic.  
 OS Mus sp.  
 XX

PN WO9951743-A1.  
 XX 14-OCT-1999.  
 XX 02-APR-1999; 99WO-JP001768.  
 XX 03-APR-1998; 98JP-00091850.  
 XX (CHUS ) CHUGAI SEIYAKU KK.  
 XX Sato K, Adachi H, Yabuta N;  
 PI WPI; 1999-620204/53.  
 XX P-PSDB; AAY52762.  
 XX Humanised antibody recognizing human tissue factor, used for treatment of  
 PT disseminated intravascular coagulation.  
 XX  
 XX Example 1; Page 192; 291pp; Japanese.  
 XX  
 CC The present invention describes chimeric antibody (Ab) heavy (H) chains  
 CC containing the variable region of the H chain of a mouse monoclonal Ab  
 CC recognising human tissue factor (hTF) and the constant region of the H  
 CC chain of a human Ab. The variable region is one of six specified  
 CC sequences (which are the H chain variable regions from mouse monoclonal  
 CC Ab's ATR-2, 3, 4, 5, 7 or 8). Also described are chimeric Ab light (L) chains  
 CC containing the variable region of the L chain of a mouse monoclonal Ab  
 CC recognising human tissue factor (hTF) and the constant region of the L  
 CC chain of a human Ab, the variable region being one of six specified  
 CC sequences (which are the L chain variable regions from mouse monoclonal  
 CC Ab's ATR-2, 3, 4, 5, 7 or 8). The chimeric Ab's can be used for the treatment  
 CC and prevention of thrombotic disease, especially of disseminated  
 CC intravascular coagulation (DIC). The humanised antibody has the high hTF  
 CC binding activity of the mouse monoclonal antibody but greatly reduced  
 CC immunogenicity. AAZ33001 to AAZ33091 and Y527007 to AAY52767 represent  
 CC sequences used in the exemplification of the present invention  
 XX  
 SQ Sequence 375 BP; 96 A; 88 C; 93 G; 98 T; 0 U; 0 Other;  
 Query Match 91.0%; Score 292.2; DB 2; Length 375;  
 Best Local Similarity 94.4%; Pred. No. 2.1e-83;  
 Matches 303; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
 QY 1 GACATTGAGTACAGCCAGTCTCTGCTCCAGTCTGCATCTCTGGGAGAAAGTGTACCC 60  
 DB 55 GACATTGAGTACAGCCAGTCTCTGCTCCAGTCTGCATCTCTGGGAGAAAGTGTACCC 114  
 QY 61 ATCACATGCTGGCAAGTCAGACCATTTGATATACATGTTAGCATGGTATCAGCAGAAACCA 120  
 DB 115 ATCACATGCTGGCAAGTCAGACCATTTGATATACATGTTAGCATGGTATCAGCAGAAACCA 174  
 QY 121 GGGAAATCTCTCAGTCTGATTTATGCTGCCACCACTTGGCAGATGGGTCCCATCA 180  
 DB 175 GGGAAATCTCTCAGTCTGATTTATGCTGCCACCACTTGGCAGATGGGTCCCATCA 234  
 QY 181 AGGTTTCAGTGGCAGTGGATCTGGCACAATAATTTCTTTCAAGATCAGCAGCTACAGGCT 240  
 DB 235 AGGTTTCAGTGGTGGATCTGGCACAATAATTTCTTTCAAGATCAGCAGCTACAGGCT 294  
 QY 241 GAAGATTTGTAAATTTACTGTCAACAAAGTTTACAGTTCTCCATTCAGTTTCGGTGTCT 300  
 DB 295 GAAGATTTGTAAATTTACTGTCAACAACTTTACAGTACTCCGTACACGTTTCGGAGGG 354  
 QY 301 GGGACCAAGCTGGAGCTGAAA 321  
 DB 355 GGGACCAAGCTGGAAATAAAA 375  
 RESULT 9  
 ID AAZ51613 standard; DNA; 949 BP.  
 XX AAZ51613;  
 XX AAZ51613;



CC prophylaxis methods using such constructs are useful for the transient  
 CC protection of individuals against exposure to pathogens or toxins where  
 CC no efficient vaccines are available, for inducing the synthesis of  
 CC antibodies of a desired specificity for use in immunocompromised  
 CC individuals, and for protecting an individual against an allergic  
 CC reaction. In contrast to DNA vaccines, including anti- idiotypic vaccines,  
 CC administration of plasmid-borne genes do not involve specific activation  
 CC of the immune system in the individual. Prophylaxis against infectious  
 CC diseases takes place without any side effects such as the transfer of  
 CC infectious diseases or induction of hypersensitivity following repeated  
 CC administration. The single chain antibodies will be systemically  
 CC distributed by the body fluids and protect the individual if infection  
 CC with the pathogen occurs. The present sequence represents a portion of a  
 CC construct of the invention which encodes a single chain antibody, BUL.  
 CC BUL is reactive to the fish pathogenic rhabdovirus, VHSV. BUL is derived  
 CC from the variable regions of the VHSV-reactive murine monoclonal antibody  
 CC 3FlH10, and also contains the rainbow trout transforming growth factor  
 CC beta (tgf-beta) signal peptide at the N- terminus (to ensure secretion of  
 CC the single chain antibody) and the human kappa light chain constant  
 CC domain (used as a tag to facilitate detection) at the C-terminus  
 XX  
 XX Sequence 1135 BP; 298 A; 293 C; 273 G; 271 T; 0 U; 0 Other;

Query Match 89.5%; Score 287.4; DB 4; Length 1135;  
 Best Local Similarity 93.5%; Pred. No. 1.2e-81;  
 Matches 300; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
 QY 1 GACATTCAGATGACCCAGTCTCTCGCTCCAGTCTGCATCTCTGGGAGAAAGTGTACCC 60  
 DB 478 GACATTCGAGCTCACCAGTCTCTCGCTCCAGTCTGCATCTCTGGGAGAAAGTGTACCC 537  
 QY 61 ATCACATGCTCGGCAAGTCAGACCATTTGATACATGTTAGCATGTTATCAGCAGAAACCA 120  
 DB 538 ATCACATGCTCGGCAAGTCAGACCATTTGATACATGTTAGCATGTTATCAGCAGAAACCA 597  
 QY 121 GGGAAATCTCTCAGCTCCTGATTTATGCTGCCAACAACTTGGCAGATGGGGTCCCATCA 180  
 DB 598 GGGAAATCTCTCAGCTCCTGATTTATGCTGCCAACAACTTGGCAGATGGGGTCCCATCA 657  
 QY 181 AGGTTTCAGTGGCAGTGGATCTGGCACAATAATTTCTTTCAAGATCAGCAGCTACAGGCT 240  
 DB 658 AGGTTTCAGTGGTGGATCTGGCACAATAATTTCTTTCAAGATCAGCAGCTACAGGCT 717  
 QY 241 GAAGATTTTGTAATTTATTACTGTCAACAAGTTTACAGTTTCCCAATTCAGCTTCGGTGTCT 300  
 DB 718 GAAGATTTTGTAAGTTATTACTGTCAACAATTTTACAGTACTCCGTACACGTTTCGGAGGG 777  
 QY 301 GGGACCAAGCTCGAGCTGAAA 321  
 DB 778 GGGACCAAGCTCGAGATCAAA 798

RESULT 11  
 AAT04179  
 ID AAT04179 standard; cDNA to mRNA; 1300 BP.

XX AC AAT04179;  
 XX DT 09-MAY-1996 (first entry)  
 XX DE C179Fv-PP coding sequence.  
 XX KW Antibody; human; influenza type A virus; H1N1; H2N2; H3N2; HA; diagnosis;  
 XX KW haemagglutinin; variable heavy chain; therapy; ds.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 XX CDS 40..468  
 XX FT /\*tag= a  
 XX FT /product= "variable heavy chain region"  
 XX FT 106..465  
 XX FT misc\_feature  
 XX FT /\*tag= c

FT CDS  
 FT 523..1290  
 FT /\*tag= b  
 FT /product= "variable light chain-Fc fusion protein"  
 FT 601..902  
 FT /\*tag= d  
 FT /product= "variable light chain"  
 FT 928..1101  
 FT /\*tag= e  
 FT /note= "Fc binding domain-like structure"  
 FT 1102..1275  
 FT /\*tag= f  
 FT /note= "Fc binding domain-like structure"  
 XX EP675199-A2.  
 XX 04-OCT-1995.  
 XX 14-MAR-1995; 95EP-00301664.  
 XX 30-MAR-1994; 94JP-00082693.  
 XX (TAKI ) TAKARA SHUZO CO LTD.  
 XX Yoshinobu O, Atsushi O, Hirofumi Y, Takashi T, Ikunoshin K;  
 XX WPI; 1995-338286/44.  
 XX P-PSDB; AAR92828, AAR92829.  
 XX Gene encoding variable region of anti-human influenza A type virus  
 XX antibody - useful for prodn. of artificial antibodies.  
 XX Example 4; Page 32-35; 42pp; English.  
 CC This sequence encodes the C179Fv-PP fusion polypeptide. The encoded  
 CC sequence is an anti-human influenza A type virus antibody. The antibody  
 CC recognises the stem region of the haemagglutinin (HA) molecule of the  
 CC H1N1 and H2N2 subtypes of human influenza A type virus, and shows  
 CC neutralisation activity against these two subtypes. The antibody shows no  
 CC recognition of the H3N2 subtype. Artificial antibodies (such as this) and  
 CC polypeptides are useful in the diagnosis and treatment of human  
 CC influenza. As the antibodies recognise the stem region of the HA  
 CC molecule, the influenza virus will be recognised even if the HA molecule  
 CC changes. This provides an advantage over current vaccines, as the virus  
 CC periodically alters it's HA molecule  
 XX Sequence 1300 BP; 393 A; 319 C; 289 G; 299 T; 0 U; 0 Other;  
 Query Match 89.4%; Score 287; DB 2; Length 1300;  
 Best Local Similarity 93.7%; Pred. No. 1.7e-81;  
 Matches 299; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 GACATTCAGATGACCCAGTCTCTCGCTCCAGTCTGCATCTCTGGGAGAAAGTGTACCC 60  
 DB 589 GACATTCGAGCTCACCAGTCTCTCGCTCCAGTCTGCATCTCTGGGAGAAAGTGTACCC 648  
 QY 61 ATCACATGCTCGGCAAGTCAGACCATTTGATACATGTTAGCATGTTATCAGCAGAAACCA 120  
 DB 649 ATCACATGCTCGGCAAGTCAGACCATTTGATACATGTTAGCATGTTATCAGCAGAAACCA 708  
 QY 121 GGGAAATCTCTCAGCTCCTGATTTATGCTGCCAACAACTTGGCAGATGGGGTCCCATCA 180  
 DB 709 GGGAAATCTCTCAGCTCCTGATTTATGCTGCCAACAACTTGGCAGATGGGGTCCCATCA 768  
 QY 181 AGGTTTCAGTGGATCTGGCACAATAATTTCTTTCAAGATCAGCAGCTACAGGCT 240  
 DB 769 AGGTTTCAGTGGTGGATCTGGCACAATAATTTCTTTCAAGATCAGCAGCTACAGGCT 828  
 QY 241 GAAGATTTTGTAATTTATTACTGTCAACAAGTTTACAGTTTCCCAATTCAGCTTCGGTGTCT 300  
 DB 829 GAAGATTTTGTAAGTTATTACTGTCAACAATTTTACAGTACTCCGTGACAGTTTCGGTGA 888  
 QY 301 GGGACCAAGCTCGAGCTGA 319

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Db      889 GGCACCAAGCTGGAGTCGA 907
|||||
RESULT 12
ADZ51605
ID      ADZ51605 standard; DNA; 949 BP.
XX
AC      ADZ51605;
XX
DT      30-JUN-2005 (first entry)
XX
High-functioning protein related DNA SEQ ID NO 106.
DE
KW      cytostatic; hypotensive; nucleic acid library; cancer; neoplasm;
KW      hypertension; cardiovascular disease; ds; gene.
XX
OS      Unidentified.
XX
PN      WO2005035751-A1.
XX
PD      21-APR-2005.
XX
PF      15-OCT-2004; 2004WO-JP015290.
XX
PR      15-OCT-2003; 2003JP-00355702.
XX
PA      (UYKE-) UNIV KEIO.
XX
PI      Yanagawa H, Tabata N, Kojoh K;
XX
DR      WPI; 2005-346216/35.
DR      P-PSDB; ADZ51606.
XX
Selecting a high-functioning protein which is useful for treating cancer
PT      and hypertension, comprises selecting a protein interacting with a target
PT      molecule.
XX
PS      Disclosure; SEQ ID NO 106; 92pp; Japanese.
XX
The invention relates to a method of selecting a high-functioning protein
CC      which comprises constructing a protein-coding DNA library, transcribing
CC      DNAs, attaching a spacer to the 3' end of transcribed RNAs and
CC      constructing a library of molecules assigned to genotype and phenotype in
CC      a cell-free translation system, treating the library of assigned
CC      molecules, binding an assigned molecule to a target molecule and
CC      amplifying nucleic acid. The method is useful for selecting a high-
CC      functioning protein by selecting a protein interacting with a target
CC      molecule. The method is useful for manufacturing a protein which
CC      interacts with a target molecule. The single stranded antibodies are
CC      useful for treating cancer and hypertension. The method is rapid and
CC      efficient. The present sequence represents a high-functioning protein
CC      related DNA.
XX
SQ      Sequence 949 BP; 247 A; 221 C; 261 G; 220 T; 0 U; 0 Other;

Query Match      89.0%; Score 285.8; DB 14; Length 949;
Best Local Similarity 93.1%; Pred. No. 3.6e-81;
Matches 299; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY      1 GACATTCAGATCACCAGCTCTCTGCTCCAGTCGATCTCTGGAGAAAGTGTACCC 60
Db      552 GACATTCAGATCAGACAGTTTCTGCTCCAGTTTGTGATCTTTGGAGAAAGTGTCAATC 611
QY      61 ATCATATGCTGGCAGTCAGACCATTTGATATAGTGTAGCATGGTATCAGACGAAACCA 120
Db      612 ATCATATGCTGGCAGTCAGACCATTTGATATAGTGTAGCATGGTATCAGACGAAACCA 671
QY      121 GGGAAATCTCTCAGCTCTGATTTATGTGTCACCACTTGGCAGATGGGTGCCATCA 180
Db      672 GGGAAATCTCTCAGCTCTGATTTATGTGTCACCACTTGGCAGATGGGTGCCATCA 731
QY      181 AGGTTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTTTCAAGATCAGAGCCTACAGGCT 240

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Db      732 AGGTTTCAGTGGTGTAGTGGATCTGGCACAAAATTTCTTTCAAGATCAGAGCCTACAGGCT 791
QY      241 GAAGATTTTGTAAATTTACTGTCAACAAAGTTTACAGTTCTCTCATTTCAGGTTTCGGTGCT 300
Db      792 GAAGATTTTGTAAAGTTTACTGTCAACAACTTTACAGTACTCGTGGAGCTTCGGTGGA 851
QY      301 GGGACCAAGCTGGAGCTGAAA 321
Db      852 GGCACCAAGCTGGAAATCAAA 872

RESULT 13
AAT04180
ID      AAT04180 standard; cDNA to mRNA; 1228 BP.
XX
AC      AAT04180;
XX
DT      09-MAY-1996 (first entry)
XX
scFv-PP coding sequence.
DE
KW      Antibody; human; influenza type A virus; H1N1; H2N2; H3N2; HA; diagnosis;
KW      haemagglutinin; variable heavy chain; therapy; ds.
XX
OS      Synthetic.
XX
FH      Location/Qualifiers
FT      CDS
FT      40..1218
FT      /tag= a "scFv-PP"
FT      /product=
FT      106..471
FT      /tag= b
FT      /product= "variable heavy chain"
FT      529..830
FT      /tag= c
FT      /product= "variable light chain"
FT      856..1029
FT      /tag= d
FT      /note= "Fc binding domain-like structure"
FT      1030..1203
FT      /tag= e
FT      /note= "Fc binding domain-like structure"
XX
EP675199-A2.
XX
PD      04-OCT-1995.
XX
PF      14-MAR-1995; 95EP-00301664.
XX
PR      30-MAR-1994; 94JP-00082693.
XX
PA      (TAKI ) TAKARA SHUZO CO LTD.
XX
PI      Yoshinobu O, Atsushi O, Hirofumi Y, Takashi T, Ikunoshin K;
XX
WPI; 1995-338286/44.
DR      P-PSDB; AAR82835.
XX
Gene encoding variable region of anti-human influenza A type virus
PT      antibody - useful for prodn. of artificial antibodies.
XX
Example 4; Page 36-38; 42pp; English.
XX
This sequence encodes the scFv-PP fusion polypeptide. The encoded
CC      sequence is an anti-human influenza A type virus antibody. The antibody
CC      recognises the stem region of the haemagglutinin (HA) molecule of the
CC      H1N1 and H2N2 subtypes of human influenza A type virus, and shows
CC      neutralisation activity against these two subtypes. The antibody shows no
CC      recognition of the H3N2 subtype. Artificial antibodies (such as this) and
CC      polypeptides are useful in the diagnosis and treatment of human
CC      influenza. As the antibodies recognise the stem region of the HA
CC      molecule, the influenza virus will be recognised even if the HA molecule

```



CC which comprises constructing a protein-coding DNA library, transcribing  
CC DNAs, attaching a spacer to the 3' end of transcribed RNAs and  
CC constructing a library of molecules assigned to genotype and phenotype in  
CC a cell-free translation system, treating the library of assigned  
CC molecules, binding an assigned molecule to a target molecule and  
CC amplifying nucleic acid. The method is useful for selecting a high-  
CC functioning protein by selecting a protein interacting with a target  
CC molecule. The method is useful for manufacturing a protein which  
CC interacts with a target molecule. The single stranded antibodies are  
CC useful for treating cancer and hypertension. The method is rapid and  
CC efficient. The present sequence represents a high-functioning protein  
CC related DNA.  
XX

QY Sequence 949 BP; 248 A; 218 C; 259 G; 224 T; 0 U; 0 Other;

Query Match 88.0%; Score 282.6; DB 14; Length 949;

Best Local Similarity 92.5%; Pred. No. 3.8e-80;

Matches 297; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGTCATCTCTGGAGAAAGTGCACC 60

Db |||||||||||| |||||||||||| |||||||||||| |||||||||||| ||||||||||||  
552 GACATTCAGATGACACAGATTTCTGCTCCAGTCTGCAATTTCTGGAGAAAGTGCATC 611

QY 61 ATCAGATGCTGCAAGTCAGACCATGTATACATGGTTAGCATGGTATCAGCAGAAACCA 120

Db |||||||||||| |||||||||||| |||||||||||| |||||||||||| ||||||||||||  
612 ATCAGATGCTGCAAGTCAGACCATGTGGTACATGGTTAGCATGGTATCAACAGAAACCA 671

QY 121 GGGAAATCTCTCAGCTCTCTGATTTATGCTGCCACCAACTTGGCAGATGGGTCCCATCA 180

Db |||||||||||| |||||||||||| |||||||||||| |||||||||||| ||||||||||||  
672 GGGAAATTTCTCAGCTCTCTGATTTATGCTGCCAACCCAGCTGGGCAGATGGGTCCCATCA 731

QY 181 AGTTTCAGTGGCAGTGGATCTGGCACAATAATTTCTTTCAAGATCAGACCTACAGGCT 240

Db |||||||||||| |||||||||||| |||||||||||| |||||||||||| ||||||||||||  
732 AGTTTCAGTGGTGGTGGATTTGGCACAATAATTTCTTTCAAGATCAGACCTACAGGCT 791

QY 241 GAAGATTTTGTAAATTTACTCTCAACAGTTTACAGTTCTCCATTACGTTCCGGTGT 300

Db |||||||||||| |||||||||||| |||||||||||| |||||||||||| ||||||||||||  
792 GAAGATTTTGTAAAGTTTACTCTCAACAACTTTACAGTACTCCGTGGACGTTCCGGTGA 851

QY 301 GGGACCAAGCTGGAGCTGAAA 321

Db |||||||||||| ||||  
852 GGCACCAAGCTGGAAATCAAA 872

Search completed: April 18, 2006, 18:33:15

Job time : 460 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
3947.084 Million cell updates/sec

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Perfect score: 321  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 1: gb\_est1.\*
- 2: gb\_est2.\*
- 3: gb\_est3.\*
- 4: gb\_hic.\*
- 5: gb\_est4.\*
- 6: gb\_est5.\*
- 7: gb\_est6.\*
- 8: gb\_est7.\*
- 9: gb\_gss1.\*
- 10: gb\_gss2.\*
- 11: gb\_gss3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	270.8	84.4	700	10 AG319984	AG319984 Mus muscu
2	248.2	77.3	553	2 BE309991	BE309991 601091717
3	237	73.8	603	6 CF111270	CF111270 Shultzomi
4	229.8	71.6	896	2 BG969371	BG969371 602836854
5	226.6	70.6	939	4 AK002514	AK002514 Mus muscu
6	226.6	70.6	964	2 BG966302	BG966302 602832780
7	221.8	69.1	577	2 BE305476	BE305476 601099542
8	221.8	69.1	721	2 BG967689	BG967689 602833496
9	221.8	69.1	757	6 CB987347	CB987347 AGENCOURT
10	221.2	68.9	727	9 BZ120378	BZ120378 CH230-317
11	220.2	68.6	599	2 BE287315	BE287315 601093986
12	220.2	68.6	683	6 CB984699	CB984699 AGENCOURT
13	220.2	68.6	691	2 BE307937	BE307937 601096061
14	220.2	68.6	829	7 CO575799	CO575799 AGENCOURT
15	220.2	68.6	867	2 BG754732	BG754732 602714301
16	218.6	68.1	422	1 AW407904	AW407904 UI-HF-BLO
17	218.6	68.1	472	6 CD702614	CD702614 EST19139
18	218.6	68.1	525	3 BP422398	BP422398 BP422398
19	218.6	68.1	525	6 CD709957	CD709957 EST26484
20	218.6	68.1	588	6 CD709469	CD709469 EST25996
21	218.6	68.1	616	6 CD709768	CD709768 EST28295
22	218.6	68.1	697	6 CD699896	CD699896 EST16420

23	218.6	68.1	805	3	BI454240	BI454240 603170666
24	218.6	68.1	823	2	BF580331	BF580331 602097072
25	217.2	67.7	754	2	BG967635	BG967635 602833433
26	217	67.6	431	1	AW406886	AW406886 UI-HF-BLO
27	217	67.6	460	1	AW405906	AW405906 UI-HF-BLO
28	217	67.6	485	1	AJ548351	AJ548351 AJ548351
29	217	67.6	493	1	AW405753	AW405753 UI-HF-BLO
30	217	67.6	499	6	CD685478	CD685478 EST1998 h
31	217	67.6	522	3	BP421572	BP421572 BP421572
32	217	67.6	568	6	CD710582	CD710582 EST27109
33	217	67.6	693	6	CD684441	CD684441 EST961 hu
34	217	67.6	724	6	CB959008	CB959008 AGENCOURT
35	217	67.6	743	6	CB957909	CB957909 AGENCOURT
36	217	67.6	769	6	CB957759	CB957759 AGENCOURT
37	217	67.6	793	6	CB987506	CB987506 AGENCOURT
38	217	67.6	799	6	CB984750	CB984750 AGENCOURT
39	217	67.6	842	6	CB986591	CB986591 AGENCOURT
40	217	67.6	886	2	BG756818	BG756818 602710291
41	217	67.6	933	2	BG533956	BG533956 603553057
42	217	67.6	1100	2	BF663472	BF663472 602144635
43	215.4	67.1	471	6	CD702236	CD702236 EST18760
44	215.4	67.1	495	6	CD708794	CD708794 EST25321
45	215.4	67.1	574	6	CD710508	CD710508 EST27035

ALIGNMENTS

RESULT 1	AG319984	AG319984	Mus musculus molossinus DNA, clone:MSMg01-105L04.T7, genomic survey sequence.	700 bp	DNA	linear	GSS 18-DEC-2004
LOCUS	AG319984	AG319984	GSS.				
ACCESSION	AG319984.1	GI:47892941					
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
PUBMED							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
COMMENT							
PRIMERS							
Sequencing							
Vector							
R.Site 1							
R.Site 2							
FEATURES							
source							

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/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSNg01-105L04.T7"
/sex="male"
/tissue_type="mixture of kidney and
/clouse_lib="MSNg01 Mouse Male BAC L
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## ORIGIN

Query Match	84.4%	Score 270.8	DB 10	Length 700
Best Local Similarity	95.9%	Prod. No. 2.1e-72		
Matches 278	Conservative 0	Mismatches 12	Indels 0	Gaps 0
1	GACATTTCAGATGACCCAGCTCTCTGGCTCCCGAGTCTGCATCTCTGGGAGAAAGTGTCAAC	60		
91	GACATTTCAGATGACCCAGCTCTCTGGCTCCCGAGTCTGCATCTCTGGGAGAAAGTGTCAAC	150		
61	ATCACATGCCCTGGCAAGTCAGACCAATTGATACATGTTAGCATGGTATCAGCAGAAACCA	120		
151	ATCACATGCCCTGGCAAGTCAGACCAATTGGTACATGGTTAGCATGGTATCAGCAGAAACCA	210		
121	GGGAAATCTCTTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA	180		
211	GGGAAATCTCTTCAGCTCCTGATTTATGCTGCCACCAAGTGGGAGATGGGGTCCCATCA	270		
181	AGGTCAGTGGCAGTGATCTGGCACAAAATTTTCTTCAGATTCAGCAGCCTACAGCT	240		
271	AGGTCAGTGGTGTGATCTGGCACAAGTTTCTTCAGATTCAGCAGCCTACAGCT	330		
241	GAAGATTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCAAC	290		
331	GAAGATTTGCAAGTTATTCTGTCAACAACATTACAGTACTCTCTCAAC	380		

## RESULT 2

BE309991	BE309991	553 bp	mRNA	linear	EST 26-OCT-2000					
LOCUS	601091717F1	NCI_CGAP_Mam5	Mus musculus	cdna clone	IMAGE:3486245 5',					
DEFINITION	mRNA sequence.									
ACCESSION	BE309991									
VERSION	BE309991.1	GI:9169034								
KEYWORDS	EST.									
SOURCE	Mus musculus	(house mouse)								
ORGANISM	Mus musculus									
	Eukaryota;	Metazoa;	Chordata;	Craniata;	Vertebrata; Euteleostomi;					
	Mammalia;	Eutheria;	Euarchontoglires;	Glires;	Rodentia;					
	Sciurognathi;	Muroidea;	Muridae;	Murinae;	Mus.					
REFERENCE	1 (bases 1 to 553)									
AUTHORS	NIH-MGC	<a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a>								
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)									
JOURNAL	Unpublished (1999)									
COMMENT	Contact:	Robert Strausberg,	Ph.D.							
	Email:	cgapbs-t@mail.nih.gov								
	Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys									
	CDNA Library Preparation: Life Technologies, Inc.									
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)									
	DNA Sequencing by: Incyte Genomics, Inc.									
	Clone distribution: MGC clone distribution information can be									
	found through the I.M.A.G.E. Consortium/LNL at:									

## FEATURES

source

Email: mabn120000@as.edu  
 Average Phred score is 20 or better. All poor quality data (Phred  
 20) and vector/linker sequence has been removed.  
 High quality sequence stop: 603.

**FEATURES**  
**SOURCE**

```

/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam5"
/note="Organ: mammary; vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

```

## ORIGIN

Query Match	77.3%	Score	248.2	DB 2	Length	553				
Best Local Similarity	93.2%	Pred. No.	1.9e-65							
Matches	303	Conservative	0	Mismatches	18	Indels	4	Gaps	4	
Qy	1	GACATT	CAGATG	ACCAG-TCTCTG	GCTCC	CAGTCTG	CATCTCTGG	GAGAAAGTGT	CAC	59
Db	46	GACATT	CAGATG	ACCAGCTTCT	CTGCTCC	AGTCTG	CACTCTGG	GAGAAAGTGT	CAC	105
Qy	60	CA-TC	CATGCC	TGGCAAGT	CAGACCA	TTGATACA-TGG	TTAGCATGG	TATCAG	CAGAAA	117
Db	106	CAGTCA	CATGCC	TGGCAAGT	CAGACCA	TTGATACA-TGG	TTAGCATGG	TATCAG	CAGAAA	165
Qy	118	CAGGG	AAATCTCCT	CAGCTCCT	GTATTAT	TGCTGCC	ACCACTTGG	CAGATGGGG	TCCCA	177
Db	166	CCAGG	AAATCTCCT	CAACTCTCT	GATTTAT	TGCTGCC	AGCTTGG	CAGATGGGG	TCCCA	225
Qy	178	TC	AAGTT	CAGTGG	CAGTGG	ATCTGG	CACAAAATTTTCT	TTCAAGATC	AGCAGCT	237
Db	226	TC	AAGTT	CAGTGG	TAGTGG	ATCTGG	CACAAAATTTTCT	TTCAAGATC	AGCAGCT	285
Qy	238	GCTGA	AGATTTTGT	AAATATT	ACTGT	CAACAA-GTTT	TACAGTTCT	CCATTCAG	TTTCGG	296
Db	286	GCTGA	AGATTTTGT	AACTATT	ACTGT	CAACAACTTT	TACAGTACT	CCGTTG	GGACGTTTCGG	345
Qy	297	TGCT	GGGAC	CAAGCT	GGAGCT	GAAA				321
Db	346	TGG	AGGC	ACCAAGCT	GGAAAT	CAAA				370

RESULT 3  
CF111270

LOCUS	CFH11270	603 bp	mRNA	linear	EST 23-JUL-2003
DEFINITION	Shultzomic04521	Rat lung airway and parenchyma CDNA libraries			
	Rattus norvegicus	CDNA clone Contig432	5'	mRNA sequence.	

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FEATURES
source
Location/Qualifiers
1. .603
/organism="Rattus norvegicus"
/mol_type="mRNA"
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/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="Cont:19432"  
/sex="male"  
/tissue\_type="airway or parenchyma"  
/dev\_stage="adult"  
/clone\_lib="Rat lung airway and parenchyma cDNA libraries"  
/notes="Organ: lung; Vector: pGEM-III(-); Site: 1: Eco RI;  
Site\_2: Not I; mRNA was isolated from microdissected rat  
lung airways and parenchyma tissues."

ORIGIN

Query Match 73.8%; Score 237; DB 6; Length 603;  
Best Local Similarity 85.4%; Pred. No. 5.9e-62;  
Matches 275; Conservative 0; Mismatches 46; Indels 1; Gaps 1;  
  
QY 1 GACATTCAGATGACCCAGTCTCTCT-GCTCCCACTCTGCACTCTCTGGAGAAAGTGTCCAC 59  
DB 41 GACATCCAGATGACAGATCTCTCTGGCTCTCTGCTGCACTCTGGAGAAATTTGTCCAC 100  
  
QY 60 CATCACATGCTGGCAAGTCAGACCATTTGATATCATGTTAGCATGGTATCAGCAGAAACC 119  
DB 101 GATCACATGCTGGCAAGTCAGACCATTTGATATTTGTTAAACATGGTATCAGCAGAAACC 160  
  
QY 120 AGGGAATCTCTCAGCTCTCTGATTTATGCTGCCCACTTGGCAGATGGGTGCCATC 179  
DB 161 AGGNAATCTCTCAGCTCTCTGATCTATGTTGCAACCAAGCTTGGCAGATGGGTGCCATC 220  
  
QY 180 AAGTTTCAGTGGCAGTGGATCTGGCACAATAATTTCTTCAAGATCAGCAGCTTACAGGC 239  
DB 221 AAGTTTCAGGCGAGTAGATCTGGCACAAGTATTTCTTCAAGATCAGCAGCTTACAGGC 280  
  
QY 240 TGAAGATTTTGTAAATTTATTTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCCGGTGC 299  
DB 281 TGAAGATCTCTGGAATCTATTACTGTCTACAGAGTTATAGTACTCCGTGGAGCTTCCGTGC 340  
  
QY 300 TGGACCAAGCTGGAGCTGAAA 321  
DB 341 AGGCACCAAGCTGGAATTGAAA 362

RESULT 4  
AK002514  
LOCUS  
DEFINITION  
5', mRNA sequence. 896 bp mRNA linear EST 12-JUN-2001  
IMAGE:4971397  
  
ACCESSION  
BG969371  
VERSION  
BG969371  
KEYWORDS  
EST.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
  
REFERENCE  
1 (bases 1 to 896)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLNL0956 row: k column: 14  
High quality sequence stop: 864.  
Location/Qualifiers  
1. 896  
/organism="Mus musculus"  
/mol\_type="mRNA"

FEATURES  
source

/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4971397"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NCI CGAP Kid14"  
/notes="Organ: Kidney; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.75 Kb. Constructed by Life  
Technologies. Note: this is a NCI CGAP Library. |"  
  
ORIGIN

Query Match 71.6%; Score 229.8; DB 2; Length 896;  
Best Local Similarity 82.2%; Pred. No. 1.1e-59;  
Matches 264; Conservative 0; Mismatches 57; Indels 0; Gaps 0;  
  
QY 1 GACATTCAGATGACCCAGTCTCTCTGCCCTCCAGTCTGCACTCTCTGGAGAAAGTGTCCAC 60  
DB 79 GACATCCAGATGACTCAGTCTCCAGCTCTCCCTATCTGATCTGCGGAGAACTGTCCAC 138  
  
QY 61 ATCACATGCTGGCAAGTCAGACCATTTGATATCATGTTAGCATGGTATCAGCAGAAACCA 120  
DB 139 ATCACATGCTGGCAAGTCAGACCATTTTACAGTAATTTAGCATGGTATCAGCAGAAACAG 198  
  
QY 121 GGGAAATCTCTCAGCTCTCTGATTTATGCTGCCCACTTGGCAGATGGGTGCCATCA 180  
DB 199 GGGAAATCTCTCAGCTCTCTGATTTATGCTGCCCACTTGGCAGATGGGTGCCATCA 258  
  
QY 181 AGTTTCAGTGGCAGTGGATCTGGCACAATAATTTCTTCAAGATCAGCAGCTTACAGGC 240  
DB 259 AGTTTCAGTGGCAGTGGATCTGGCACAAGTATTTCTTCAAGATCAGCAGCTTACAGGC 318  
  
QY 241 GAAGATTTTGTAAATTTATTTACTGTCAACAAGTTTACAGTTCTCCATTCAGTTCCGGTGC 300  
DB 319 GAAGATTTTGGGAAATTTACTGTCAACATTTTGGGGTAGTCCGCTCAGTTCCGGTGC 378  
  
QY 301 GGGACCAAGCTGGAGCTGAAA 321  
DB 379 GGGACCAAGCTGGAGCTGAAA 399

RESULT 5  
AK002514  
LOCUS  
DEFINITION  
Mus musculus adult male kidney cDNA, RIKEN full-length enriched  
library, clone:0610010P20 product:immunoglobulin kappa chain  
variable 28 (V28), full insert sequence.  
  
ACCESSION  
AK002514  
VERSION  
AK002514.1  
KEYWORDS  
HTC; CAP trapper.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
  
REFERENCE  
1  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
10349636  
  
REFERENCE  
2  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
11042159  
  
REFERENCE  
3  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwara, S., Inoue, K., Tanaka, Y., Tanaka, T., Tanaka, T., Matsura, S., Kawai, J.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,



/lab host="DH10B (T1 phage-resistant)"  
/clone lib="NCI\_CGAP\_Co24"  
/notes="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.6 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

ORIGIN

Query Match 70.6%; Score 226.6; DB 2; Length 964;  
Best Local Similarity 81.6%; Pred. No. 1.1e-59;  
Matches 262; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGATCTCTGGGAGAAAGTGTCAAC 60  
Db 76 GACATTCAGATGACCTAGTCTCCAGCTCTCTATCTGTATCTGTGGGAGAAAGTGTCAAC 135

QY 61 ATCAGATGCTGGCAAGTCAGACATTTAGATATGATGTTAGCATGGTATCAGCAGAAACCA 120  
Db 136 ATCAGATGCTGGCAAGTCAGATATTTACAGTAATTTAGCATGGTATCAGCAGAAACAG 195

QY 121 GGGAAATCTCTCAGTCTCTGATTTATGTCGCCAACCAACTTTGGCAGATGGGTGCCATCA 180  
Db 196 GGGAAATCTCTCAGTCTCTGATTTATGTCGCCAACCAACTTTAGCAGATGGGTGCCATCA 255

QY 181 AGCTTCAGTGGCAGTGGATCGCACAAATTTTCTTCAAGATCAGCAGCCTACAGGCT 240  
Db 256 AGCTTCAGTGGCAGTGGATCGCACAGATTTCCCTCAAGATCAACAGCCTGCGAGTCT 315

QY 241 GAAGATTTTGTAAATTTACTGTCACAAAGTTTACAGTTCTCATTTCAGTTTCGGTGCT 300  
Db 316 GAAGATTTTGGGAATTTTCTGTCACATTTTGGGTACTCTCGTGGAGCTTCGGTGGA 375

QY 301 GGGACCAAGCTGAGCTGAAA 321  
Db 376 GGCACCAAGCTGGAATCAA 396

RESULT 7  
BE305476  
LOCUS 601099542F1 NCI\_CGAP\_Lu29 577 bp mRNA linear EST 26-OCT-2000  
DEFINITION mRNA sequence.  
ACCESSION BE305476  
VERSION BE305476.1 GI:9157223  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
1 (bases 1 to 577)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM8537 row: c column: 11  
High quality sequence stop: 576.  
Location/Qualifiers  
1..577  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="Czech II"  
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/clone="IMAGE:3492034"  
/tissue\_type="spontaneous tumor, metastatic to mammary."

FEATURES  
source

Stem cell origin."  
/lab host="DH10B"  
/clone lib="NCI\_CGAP\_Lu29"  
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 69.1%; Score 221.8; DB 2; Length 577;  
Best Local Similarity 80.7%; Pred. No. 3e-57;  
Matches 259; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGATCTCTGGGAGAAAGTGTCAAC 60  
Db 56 GACATTCAGATGACTCAGTCTCCAGCTCTCTATCTGATCTGTGGGAGAAAGTGTCAAC 115

QY 61 ATCAGATGCTGGCAAGTCAGACATTTAGATATGATGTTAGCATGGTATCAGCAGAAACCA 120  
Db 116 ATCAGATGCTGGCAAGTCAGATATTTACAGTTATTTAGCATGGTATCAGCAGAAACAG 175

QY 121 GGGAAATCTCTCAGTCTCTGATTTATGTCGCCAACCAACTTTGGCAGATGGGTGCCATCA 180  
Db 176 GGGAAATCTCTCAGTCTCTGATTTATGTCGCCAACCAACTTTAGCAGATGGGTGCCATCA 235

QY 181 AGCTTCAGTGGCAGTGGATCGCACAAATTTTCTTCAAGATCAGCAGCCTACAGGCT 240  
Db 236 AGCTTCAGTGGCAGTGGATCGCACAGATTTTCTTGAAGATCAACAGCCTGCGAGCT 295

QY 241 GAAGATTTTGTAAATTTACTGTCACAAAGTTTACAGTTCTCATTTCAGTTTCGGTGCT 300  
Db 296 GAAGATTTTGGGAGTTTATTTACTGTCACATCATTTATGGTACTCTCCGACGTTTCGGTGGA 355

QY 301 GGGACCAAGCTGAGCTGAAA 321  
Db 356 GGCACCAAGCTGGAATCAA 376

RESULT 8  
BE305476  
LOCUS 602833496F1 NCI\_CGAP\_Co24 721 bp mRNA linear EST 12-JUN-2001  
DEFINITION mRNA sequence.  
ACCESSION BE305476  
VERSION BE305476.1 GI:14355326  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
1 (bases 1 to 721)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM10999 row: p column: 23  
High quality sequence stop: 720.  
Location/Qualifiers  
1..721  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4988038"

FEATURES  
source





found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: NDCM132 row: j column: 05  
 High quality sequence stop: 547.

## FEATURES

1. ...683  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGS:30325948"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH MGC 184"  
 /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site 1:  
 SfiI (ggcattatgcc); Site 2: SfiI (ggcgctcgccg).  
 Library is oligo-dT primed and directionally cloned. cDNA  
 was prepared from a glandular pool of tissues from thyroid  
 parathyroid, adrenal, cortex and pineal gland. 5' and 3'  
 adaptors are used in cloning as follows: 5' adaptor  
 sequence: 5'-CACGCCCATATGCC-3' and 3' adaptor sequence:  
 5'-ATTATGAGGCCGGCGGCACATG-3' (30)BN-3' (where B = A,  
 C, G and N = A, C, G, or T). Average insert size 1.38  
 kb (range 0.6-3.5 kb). 15/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH MGC Library."

## ORIGIN

Query Match	68.6%;	Score	220.2;	DB	6;	Length	683;
Best Local Similarity	80.4%;	Prod. No.	9.8e-57;				
Matches	258;	Conservative	0;	Mismatches	63;	Indels	0;
Gaps	0;						

  

1	GACATTCAGATGACCCAGCTCTCGCTCCAGTCGTGATCTCTCGGAGAAAGTGTACCC	60
yy		
bb		
90	GACATCCAGTTGACCCAGCTCTCCATCTTCTCTGTCATCTATAGGACAGAGTCA	149
yy		
bb		
61	ATCACATGCTCGGCAAGTCAGACCAATTGATACATGGTTAGCATGGTATCAGCAGAAAAACA	120
yy		
bb		
150	ATCACTTGCGGGCCAGTCAGGGCATTAGCAGTTATTAGCTGGTATCAGCAAAAAATCA	209
yy		
bb		
121	GGGAATCTCTCAGCTCTCGATTTATGCTGCCACAACTGGCGAGATGGGGTCCCATCA	180
yy		
bb		
210	GGGAAAGCCCCCTAAAGCTCTGATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCA	269
yy		
bb		
181	AGSTTCAGTGGCGAGTGGATCTCGCACAAATTTTCTTTCAAGATCAGCAGGCTCAGGCT	240
yy		
bb		
270	AGSTTCAGGCGGAGTGGATCTGGACAGAGTTCACTCTCACACTCAGCAGGCTCGAGGCT	329
yy		
bb		
241	GAAGATTTTGTAAATTTATTACTGTCTCAACAAAGTTTACAGTTTCTTCCATTCA	300
yy		
bb		
330	GAAGATTTTGGCAACTTATTACTGTCAACAACTTTACAGTTACCTTTAC	389
yy		
bb		
301	GGGACCAAGCTGGAGCTGAAA	321
yy		
bb		
390	GGGACCCAGGTTGGAGATCAAA	410
yy		
bb		

RESULT 13	BE307937	691 bp	linear	EST 26-OCT-2000
LOCUS	BE307937		mRNA	
DEFINITION	6010956061F1 NCI_CGAP_Mam5	Mus musculus	cdna clone	IMAGE:3490647 5',
			mRNA sequence.	
ACCESSION	BE307937			
VERSION	BE307937.1	GI:9163812		
KEYWORDS	EST.			
SOURCE	Mus musculus			
ORGANISM	Mus musculus (house mouse)			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;			
	Sciurognathi; Murioidea; Muridae; Murinae; Mus.			
	1 (bases 1 to 691)			
REFERENCE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .			
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)			
TITLE	Unpublished (1999)			
JOURNAL				

**COMMENT**

Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@email.nih.gov  
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM8533 row: i column: 16  
High quality sequence spot: 568.

## FEATURES

source

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1. .691
/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3490647"
/tissue_type="tumor, gross tissue stages="7 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: Site 2; NotI; Cloned undirectly. Library constructed by Life Technologies. Cloning provided samples: Lothar Hennig."

```

## ORIGIN

Query Match	68.6%	Score	220.2	DB 2	Length	691			
Best Local Similarity	80.4%	Pred. No.	9.8e-57						
Matches	258	Conservative	0	Mismatches	63	Indels	0	Gaps	0
Qy	1	GACATTCAGATGACCCAGTCTCTGCCTCCAGTCTCGATCTCTGGGAGAAAGTGTACCC	60						
Db	72	GATCCAGATGACTCAGTCTCAGCCTCCCTATCTGTATCTGTGGGAGAACTGTGTACCC	131						
Qy	61	ATCACATGCCCTGGCAGATCGACGATTCATACATGTTAGCATGGTATCAGCAGAAAAACA	120						
Db	132	ATCACATGTCGAACAGTGAGATATTTACAGTAATTTAGCATGGTATCAGCAGAAAAACAG	191						
Qy	121	GGGAAATCTCCTCAGCTCTCGATTTATGCTGCCACCAACTTTGGCAGATGGGGTCCCATCA	180						
Db	192	GGAAAACTCTCCTCAGCTCCTGGTCTATGCTGTGCAACAAACTTTAGCAGACGGTGTGCCATCA	251						
Qy	181	AGGTTTCAGTGGCAGTGGATCTGCGACAAAATTTCTTTCAAGATCAGCAGCTACAGGCT	240						
Db	252	AGGTTTCAGTGGCAGTGGATCAGGACACAGTATTCATAACGATCAACAGCCTCGAGTCT	311						
Qy	241	GAAGATTTTTGTAATTTATTACTGTGCAACAAAGTTTTACAGTTCTCCATTTCAAGTTCGGTGCT	300						
Db	312	GAGATTTTTGGGAGTTATTATTGTCAACATTTTTTGGGGTACTCGGTACACGTTCCGGAGG	371						
Qy	301	GGGACCAAGCTGGAGCTGAAA	321						
Db	372	GGGACCAAGCTGGGAATAAAA	392						

RECIT.T 14

Accession	CO575799	829 bp	mRNA	linear	EST 19-JUL-2004
LOCUS	AGENCOURT_28538931	NIH_MGC_249	Rattus norvegicus	cdna clone	
DEFINITION	IMAGE:7375130	5', mRNA sequence.			
ACCESSION	CO575799				
VERSION	CO575799.1	GI:50388428			
KEYWORDS	EST.				
SOURCE	Rattus norvegicus	(Norway rat)			
ORGANISM	Rattus norvegicus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;				
	Sciurognathi; Muridae; Murinae; Rattus.				
REFERENCE	1 (bases 1 to 829)				
AUTHORS	NIH-MGC	<a href="http://mgc.ncl.nih.gov/">http://mgc.ncl.nih.gov/</a> .			



**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgabbs-r@mail.nih.gov  
 Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical  
 College of Wisconsin  
 cDNA Library Preparation: Open Biosystems  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM1525 row: b column: 24  
 High quality sequence stop: 632.  
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 /clone="IMAGE:7375130"  
 /lab\_host="DH10B Tona"  
 /clone\_lib="NIH\_MGC\_249"  
 /note="Organ: spleen; Vector: pExpress-1; Site 1: EcoRV;  
 Site 2: NotI; RNA obtained from testis tissue of 8 wk old  
 animal. Tissues were snap-frozen and kept at -80C before  
 RNA extraction and purification (Tri-reagent method). cDNA  
 was primed using oligo-dT primer:  
 5'-pGACTAGTCTAGATCGAGCGGCCCC(T)25-3' and cloned into  
 the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb  
 resulted in an average insert size of 1.4 kb. This primary  
 library is normalized ( primary library is NIH MGC 248)  
 and was constructed by Express Genomics (Frederick, MD).  
 Note: this is a NIH\_MGC library"

**ORIGIN**  
 Query Match 68.6%; Score 220.2; DB 7; Length 829;  
 Best Local Similarity 80.4%; Pred. No. 1e-56;  
 Matches 258; Conservative 0; Mismatches 63; Indels 0; Gaps 0;  
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**RESULT 15**  
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 LOCUS 602714301F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4854409 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BG754732

**VERSION** BG754732.1 GI:14065385  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
**REFERENCE** 1 (bases 1 to 867)  
**AUTHORS** NIH-MGC http://mgc.nci.nih.gov/.  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLCM1702 row: a column: 02  
 High quality sequence stop: 805.  
**FEATURES** Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:4854409"  
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 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_48"  
 /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

**ORIGIN**  
 Query Match 68.6%; Score 220.2; DB 2; Length 867;  
 Best Local Similarity 80.4%; Pred. No. 1.1e-56;  
 Matches 258; Conservative 0; Mismatches 63; Indels 0; Gaps 0;  
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 DB 205 GGGAAAGCTCTTAAGCTCTGATCTATGATGCTCCAGTTTGGAAAGTGGGGTCCCTTCA 264  
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 DB 265 AGGTTTCAGCGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGACGCT 324  
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 DB 325 GAAGATTTTGCACACTTATTACTGTCAACAGTTTATTAATTACCTCTCACTTTGGCGGA 384  
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 DB 385 GGGACCAAGCTGGAGATCAAA 405

Search completed: April 18, 2006, 20:05:21  
 Job time : 3808 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2006, 18:26:07 ; Search time 167 Seconds  
(without alignments)  
3416.750 Million cell updates/sec

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	321	100.0	321	3	US-09-293-854-1
3	293.8	91.5	375	3	US-09-647-468-12
4	293.8	91.5	375	3	US-09-647-468-13
5	287	89.4	1228	2	US-08-401-908-35
6	287	89.4	1300	2	US-08-401-908-34
7	278.4	86.7	312	2	US-07-789-344A-7
8	277.4	86.4	295	2	US-08-401-908-4
9	239.4	74.6	366	3	US-09-140-084-22
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15	239.4	74.6	366	3	US-09-009-388C-21
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28 228.2 71.1 979 3 US-09-770-916-3 Sequence 3, Appli  
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31 226.6 70.6 714 3 US-09-472-087-62 Sequence 62, Appli  
32 226.6 70.6 754 2 US-07-958-140-1 Sequence 1, Appli  
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35 226.6 70.6 1644 2 US-08-792-824-11 Sequence 11, Appli  
36 226.6 70.6 1672 2 US-08-792-824-2 Sequence 2, Appli  
37 226.6 70.6 4435 2 US-08-792-824-1 Sequence 1, Appli  
38 226.6 70.6 5711 3 US-09-897-511A-8 Sequence 8, Appli  
39 226.6 70.6 6255 3 US-09-897-511A-13 Sequence 13, Appli  
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41 225 70.1 381 3 US-09-767-888-3 Sequence 3, Appli  
42 225 70.1 819 2 US-08-400-115-3 Sequence 3, Appli  
43 225 70.1 927 2 US-07-590-192-1 Sequence 1, Appli  
44 223.4 69.6 381 3 US-08-933-983-6 Sequence 6, Appli  
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## ALIGNMENTS

RESULT 1  
US-08-814-806-1  
; Sequence 1, Application US/08814806  
; Patent No. 5986065  
; GENERAL INFORMATION:  
; APPLICANT: Wong, Hing C.  
; APPLICANT: Jiao, Jin-an  
; APPLICANT: Esperanza, Nieves  
; APPLICANT: Lawrence, Luepschen  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD  
; TITLE OF INVENTION: COAGULATION AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/814,806  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Corless, Peter F  
; REGISTRATION NUMBER: 33,860  
; REFERENCE/DOCKET NUMBER: 46943  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 321 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLSCULE TYPE: CDNA  
; HYPOTHETICAL: NO

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; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-814-806-1

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Best Local Similarity 100.0%; Pred. No. 1.2e-96;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 2

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US-09-293-854-1
; Sequence 1, Application US/09293854
; Patent No. 6555319
; GENERAL INFORMATION:
; APPLICANT: Wong, Hing C.
; Eperanza, Nieves
; Lawrence, Luepschen
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
; COAGULATION AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA: US/09/293,854
; APPLICATION NUMBER: US/09/293,854
; FILING DATE: 16-Apr-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/814,806
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Corless, Peter F
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 46943
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: <Unknown>
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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-293-854-1

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Best Local Similarity 100.0%; Pred. No. 1.2e-96;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 3

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; Sequence 12, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHITO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: sequence coding for L chain V region of anti-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-2
; NAME/KEY: big_peptide
; LOCATION: (1)..(54)
; NAME/KEY: mat_peptide
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; LOCATION: (55)..(375)  
; NAME/KEY: CDS  
; LOCATION: (1)..(375)  
US-09-647-468-12

Query Match 91.5%; Score 293.8; DB 3; Length 375;  
Best Local Similarity 94.7%; Pred. No. 1.4e-87;  
Matches 304; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCATCTCTGGGAGAAAGTGTCAAC 60  
DB 55 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCATCTCTGGGAGAAAGTGTCAAC 114  
QY 61 ATCATATGCTGCGAAGTCAGACCAATGATACATGGTTAGCATGGTATCAGCAGAAACCA 120  
DB 115 ATCATATGCTGCGAAGTCAGACCAATGATACATGGTTAGCATGGTATCAGCAGAAACCA 174  
QY 121 GGGAAATCTCTCAGCTCTGATGTTATGCTGCCACCAACTTTGGCAGATGGGTCCTCATCA 180  
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RESULT 4  
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; Sequence 13, Application US/09647468  
; Patent No. 6677436  
; GENERAL INFORMATION:  
; APPLICANT: SATO, KOH  
; APPLICANT: ADACHI, HIDEKI  
; APPLICANT: YABUTA, NAOKIHO  
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND  
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY  
; FILE REFERENCE: 053466/0289  
; CURRENT APPLICATION NUMBER: US/09/647,468  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR FILING DATE: 1999-04-02  
; PRIOR APPLICATION NUMBER: JF 10-91850  
; PRIOR FILING DATE: 1998-04-03  
; NUMBER OF SEQ ID NOS: 183  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 375  
; TYPE: DNA  
; ORGANISM: Mus sp.  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide  
; OTHER INFORMATION: sequence coding for L chain V region of anti-TF  
; OTHER INFORMATION: mouse monoclonal antibody ATR-3  
; NAME/KEY: sig\_peptide  
; LOCATION: (1)..(54)  
; NAME/KEY: mat\_peptide  
; LOCATION: (55)..(375)  
; NAME/KEY: CDS  
; LOCATION: (1)..(375)  
US-09-647-468-13

Query Match 91.5%; Score 293.8; DB 3; Length 375;  
Best Local Similarity 94.7%; Pred. No. 1.4e-87;  
Matches 304; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCATCTCTGGGAGAAAGTGTCAAC 60  
DB 55 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCATCTCTGGGAGAAAGTGTCAAC 114  
QY 61 ATCATATGCTGCGAAGTCAGACCAATGATACATGGTTAGCATGGTATCAGCAGAAACCA 120  
DB 115 ATCATATGCTGCGAAGTCAGACCAATGATACATGGTTAGCATGGTATCAGCAGAAACCA 174  
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DB 235 AGTTTCAGTGGTGGATCTGGCACAATAATTTCTTTCAAGATCAGCAGCTTACAGGCT 294  
QY 241 GAAGATTTTGAATTAATTAATGCTGCAACAAAGTTTACAGTTCTCATTTCAGTTTGGTGTCT 300  
DB 295 GAAGATTTTGAATTAATTAATGCTGCAACAAAGTTTACAGTTCTCATTTCAGTTTGGTGTCT 354  
QY 301 GGGACCAAGCTGGAGCTGAAA 321  
DB 355 GGGACCAAGCTGGAATATAAA 375

RESULT 5  
US-08-401-908-35  
; Sequence 35, Application US/08401908  
; Patent No. 5684145  
; GENERAL INFORMATION:  
; APPLICANT: Yoshinobu OKUNO et al.  
; TITLE OF INVENTION: A DNA WHICH CODES FOR THE VARIABLE REGION OF  
; TITLE OF INVENTION: ANTIBODY  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/401,908  
; FILING DATE: March 10, 1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1228  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; US-08-401-908-35

Query Match 89.4%; Score 287; DB 2; Length 1228;  
Best Local Similarity 93.7%; Pred. No. 4.4e-85;  
Matches 299; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GACATTTCAGATGACCCAGCTCTCTGCTCCAGTCTGCACTCTCTGGGAGAAAGTGTCCACC 60  
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Db 517 GACATCGAGCTCACCAGTCTCTGCTCCAGTCTGCACTCTCTGGGAGAAAGTGTCCACC 576  
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QY 61 ATCACATGCTGGCAAGTCCAGACCATTTGATATACATGTTAGCATGTTATCAGCAGAAACCA 120  
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Db 577 ATCACATGCTGGCAAGTCCAGACCATTTGATATACATGTTAGCATGTTATCAGCAGAAACCA 636  
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QY 121 GGGAAATCTCTCAGCTCTGATTTATGTCGCCAACCACTTGGCAGATGGGGTCCCATCA 180  
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Db 637 GGGAAATCTCTCAGCTCTGATTTATGTCGCCAACCACTTGGCAGATGGGGTCCCATCA 696  
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QY 181 AGGTTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 240  
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Db 697 AGGTTTCAGTGGTGTGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 756  
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QY 241 GAAGATTTTGTAAATTTATTTACTGTCTCAACAAAGTTTACAGTTCTCCATTCAGTTCCGGTGT 300  
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Db 757 GAAGATTTTGTAAATTTATTTACTGTCTCAACAACTTTTACAGTACTCCGTGGAGCTTCGGTGA 816  
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QY 301 GGGACCAAGCTGGAGCTGA 319  
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Db 817 GGCACCAAGCTGGAGTGA 835  
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## RESULT 6

US-08-401-908-34  
; Sequence 34, Application US/08401908  
; Patent No. 5684146  
; GENERAL INFORMATION:  
; APPLICANT: Yoshinobu OKUNO et al.  
; TITLE OF INVENTION: A DNA WHICH CODES FOR THE VARIABLE REGION OF  
; TITLE OF INVENTION: ANTIBODY  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/401,908  
; FILING DATE: March 10, 1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1300  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear

US-08-401-908-34

Query Match 89.4%; Score 287; DB 2; Length 1300;  
Best Local Similarity 93.7%; Pred. No. 4.5e-85;  
Matches 299; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GACATTTCAGATGACCCAGTCTCTGCTCCAGTCTGCACTCTCTGGGAGAAAGTGTCCACC 60  
| | | | |  
Db 589 GACATCGAGCTCACCAGTCTCTGCTCCAGTCTGCACTCTCTGGGAGAAAGTGTCCACC 648  
| | | | |  
QY 61 ATCACATGCTGGCAAGTCCAGACCATTTGATATACATGTTAGCATGTTATCAGCAGAAACCA 120  
| | | | |  
Db 649 ATCACATGCTGGCAAGTCCAGACCATTTGATATACATGTTAGCATGTTATCAGCAGAAACCA 708  
| | | | |  
QY 121 GGGAAATCTCTCAGCTCTGATTTATGTCGCCAACCACTTGGCAGATGGGGTCCCATCA 180  
| | | | |  
Db 709 GGGAAATCTCTCAGCTCTGATTTATGTCGCCAACCACTTGGCAGATGGGGTCCCATCA 768  
| | | | |  
QY 181 AGGTTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 240  
| | | | |  
Db 769 AGGTTTCAGTGGTGTGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 828  
| | | | |  
QY 241 GAAGATTTTGTAAATTTATTTACTGTCTCAACAAAGTTTACAGTTCTCCATTCAGTTCCGGTGT 300  
| | | | |  
Db 829 GAAGATTTTGTAAATTTATTTACTGTCTCAACAACTTTTACAGTACTCCGTGGAGCTTCGGTGA 888  
| | | | |  
QY 301 GGGACCAAGCTGGAGCTGA 319  
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Db 889 GGCACCAAGCTGGAGTGA 907  
| | | | |

## RESULT 7

US-07-789-344A-7  
; Sequence 7, Application US/07789344A  
; Patent No. 5318897  
; GENERAL INFORMATION:  
; APPLICANT: Sudhir, Paul  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AND ANTIBODY  
; TITLE OF INVENTION: COMPONENTS ELICITED TO A POLYPEPTIDE ANTIGEN  
; TITLE OF INVENTION: GROUND STATE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Curtis, Morris & Safford  
; ADDRESSEE: c/o Barry Evans  
; STREET: 530 Fifth Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/789,344A  
; FILING DATE: 08-NOV-1991  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Evans, Barry  
; REGISTRATION NUMBER: 22,802  
; REFERENCE/DOCKET NUMBER: 370068-3500  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 840-3333  
; TELEFAX: (212) 840-0712  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 312 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-07-789-344A-7

Query Match 86.7%; Score 278.4; DB 2; Length 312;  
Best Local Similarity 93.3%; Pred. No. 1.7e-82;  
Matches 291; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 GACATTTCAGATGACCCAGTCTCTGCTCCAGTCTGCACTCTCTGGGAGAAAGTGTCCACC 60  
| | | | |









Search completed: April 18, 2006, 18:36:07  
Job time : 169 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2006, 18:27:07 ; Search time 574 Seconds  
(without alignments)  
4624.513 Million cell updates/sec

Title: US-10-764-140-1

Perfect score: 321

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:  
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2: /cgn2\_6/prodata/1/pubpna/US08\_PUBCOMB.seq:  
3: /cgn2\_6/prodata/1/pubpna/US09A\_PUBCOMB.seq:  
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6: /cgn2\_6/prodata/1/pubpna/US10B\_PUBCOMB.seq:  
7: /cgn2\_6/prodata/1/pubpna/US10C\_PUBCOMB.seq:  
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9: /cgn2\_6/prodata/1/pubpna/US10E\_PUBCOMB.seq:  
10: /cgn2\_6/prodata/1/pubpna/US11\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	321	100.0	321	3	US-09-293-854-1
2	321	100.0	321	3	US-09-990-586-1
3	321	100.0	321	5	US-10-293-417-1
4	321	100.0	321	6	US-10-310-113-1
5	321	100.0	321	6	US-10-230-880-1
6	321	100.0	321	8	US-10-764-140-1
7	321	100.0	321	9	US-10-618-338-1
8	293.8	91.5	375	7	US-10-462-062-12
9	292.2	91.0	375	7	US-10-462-062-13
10	239.4	74.6	366	7	US-10-738-454-21
11	239.4	74.6	366	7	US-10-738-454-22
12	239.4	74.6	724	3	US-09-237-061-1
13	236.2	73.6	366	7	US-10-738-454-23
14	236.2	73.6	1637	10	US-11-036-098-17
15	236.2	73.6	1637	10	US-11-036-098-17
16	231.4	72.1	324	7	US-10-762-629-1
17	229.8	71.6	702	9	US-10-500-696-3
18	228.2	71.1	768	9	US-10-239-656-56
19	228.2	71.1	882	9	US-10-496-059-5
20	228.2	71.1	979	3	US-09-770-916-3
21	228.2	71.1	979	9	US-10-496-059-3
22	228.2	71.1	1509	7	US-10-239-656-74
23	226.6	70.6	321	5	US-10-073-644C-3

24 226.6 70.6 321 7 US-10-239-656-7 Sequence 7, Appli  
25 226.6 70.6 387 3 US-09-791-551-51 Sequence 51, Appl  
26 226.6 70.6 714 5 US-10-153-382-18 Sequence 18, Appl  
27 226.6 70.6 714 8 US-10-612-497-62 Sequence 62, Appl  
28 226.6 70.6 714 8 US-10-776-649-62 Sequence 62, Appl  
29 226.6 70.6 714 10 US-11-085-368-18 Sequence 18, Appl  
30 226.6 70.6 5711 3 US-09-897-006-8 Sequence 8, Appl  
31 226.6 70.6 5711 3 US-09-897-511A-8 Sequence 8, Appl  
32 226.6 70.6 5711 6 US-10-397-079-8 Sequence 8, Appl  
33 226.6 70.6 5711 8 US-10-759-315-8 Sequence 8, Appl  
34 226.6 70.6 5711 9 US-10-947-881-8 Sequence 8, Appl  
35 226.6 70.6 5711 10 US-11-018-895-8 Sequence 8, Appl  
36 226.6 70.6 5711 10 US-11-036-557-8 Sequence 8, Appl  
37 226.6 70.6 6255 3 US-09-897-006-13 Sequence 13, Appl  
38 226.6 70.6 6255 3 US-09-897-511A-13 Sequence 13, Appl  
39 226.6 70.6 6255 6 US-10-397-079-13 Sequence 13, Appl  
40 226.6 70.6 6255 8 US-10-759-315-13 Sequence 13, Appl  
41 226.6 70.6 6255 9 US-10-947-881-13 Sequence 13, Appl  
42 226.6 70.6 6255 10 US-11-018-895-13 Sequence 13, Appl  
43 226.6 70.6 6255 10 US-11-036-557-13 Sequence 13, Appl  
44 225 70.1 381 3 US-09-767-888-3 Sequence 3, Appl  
45 225 70.1 381 6 US-10-289-181-3 Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-09-293-854-1  
; Sequence 1, Application US/09293854  
; Patent No. US2002018357A1  
; GENERAL INFORMATION:  
; APPLICANT: Wong, Jing C.  
; Jiao, Jin-an  
; Esperanza, Nieves  
; Lawrence, Luepschen  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD  
; COAGULATION AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION NUMBER: US/09/293,854  
; FILING DATE: 16-Apr-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Corless, Peter F  
; REGISTRATION NUMBER: 33,860  
; REFERENCE/DOCKET NUMBER: 46943  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 321 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA

;  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: <Unknown>  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-293-854-1

Query Match 100.0%; Score 321; DB 3; Length 321;  
Best Local Similarity 100.0%; Pred. No. 7e-94; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCAATCTCTGCGAGAAAGTGTCAAC 60  
DB 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCAATCTCTGCGAGAAAGTGTCAAC 60

QY 61 ATCATATGCTGCGAAGTCAGACCATTTGATATGATGTTAGCATGTTATCAGCAGAAACCA 120  
DB 61 ATCATATGCTGCGAAGTCAGACCATTTGATATGATGTTAGCATGTTATCAGCAGAAACCA 120

QY 121 GGGAAATCTCCTCAGCTCTGATTTATGCTGCGACCACTTGGCAGATGGGTGCCATCA 180  
DB 121 GGGAAATCTCCTCAGCTCTGATTTATGCTGCGACCACTTGGCAGATGGGTGCCATCA 180

QY 181 AGGTTCAAGTGGCAGTGGATCTGGCAAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240  
DB 181 AGGTTCAAGTGGCAGTGGATCTGGCAAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240

QY 241 GAAGATTTTGTAAATTTATTTACTGTCACCAAGTTTACAGTTCTCCATTACAGTTCGGTGTCT 300  
DB 241 GAAGATTTTGTAAATTTATTTACTGTCACCAAGTTTACAGTTCTCCATTACAGTTCGGTGTCT 300

QY 301 GGGACCAAGCTGGAGCTGAAA 321  
DB 301 GGGACCAAGCTGGAGCTGAAA 321

RESULT 2  
US-09-990-586-1  
; Sequence 1, Application US/0990586  
; Publication No. US20030109680A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; APPLICANT: WONG, HING C.  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
; FILE REFERENCE: 71758/46943-CIP2  
; CURRENT APPLICATION NUMBER: US/09/990,586  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(321)  
US-09-990-586-1

Query Match 100.0%; Score 321; DB 3; Length 321;  
Best Local Similarity 100.0%; Pred. No. 7e-94; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCAATCTCTGCGAGAAAGTGTCAAC 60  
DB 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCAATCTCTGCGAGAAAGTGTCAAC 60

QY 61 ATCATATGCTGCGAAGTCAGACCATTTGATATGATGTTAGCATGTTATCAGCAGAAACCA 120  
DB 61 ATCATATGCTGCGAAGTCAGACCATTTGATATGATGTTAGCATGTTATCAGCAGAAACCA 120

QY 121 GGGAAATCTCCTCAGCTCTGATTTATGCTGCGACCACTTGGCAGATGGGTGCCATCA 180  
DB 121 GGGAAATCTCCTCAGCTCTGATTTATGCTGCGACCACTTGGCAGATGGGTGCCATCA 180

QY 181 AGGTTCAAGTGGCAGTGGATCTGGCAAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240  
DB 181 AGGTTCAAGTGGCAGTGGATCTGGCAAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240

QY 241 GAAGATTTTGTAAATTTATTTACTGTCACCAAGTTTACAGTTCTCCATTACAGTTCGGTGTCT 300  
DB 241 GAAGATTTTGTAAATTTATTTACTGTCACCAAGTTTACAGTTCTCCATTACAGTTCGGTGTCT 300

QY 301 GGGACCAAGCTGGAGCTGAAA 321  
DB 301 GGGACCAAGCTGGAGCTGAAA 321

RESULT 3  
US-10-293-417-1  
; Sequence 1, Application US/10293417  
; Publication No. US20030082636A1  
; GENERAL INFORMATION:  
; APPLICANT: Wong, Hing C.  
; Jiao, Jin-an  
; Lawrence, Luepachen  
; Esperanza, Nieves  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD  
; COAGULATION AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/293,417  
; FILING DATE: 12-No. US20030082636A1-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/293,854  
; FILING DATE: 16-Apr-1999  
; APPLICATION NUMBER: 08/814,806  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Corless, Peter F  
; REGISTRATION NUMBER: 33,860  
; REFERENCE/DOCKET NUMBER: 46943  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 321 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: <Unknown>  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-293-417-1

Best Local Similarity 100.0%; Pred. No. 7e-94;  
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCAATCTCTGGGAGAAAGTGTCAACC 60  
Db 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCAATCTCTGGGAGAAAGTGTCAACC 60

Qy 61 ATCATATGCTGCGCAAGTCAGACCATTTGATGATACATGTTAGCATGGTATCAGCAGAAACCA 120  
Db 61 ATCATATGCTGCGCAAGTCAGACCATTTGATGATACATGTTAGCATGGTATCAGCAGAAACCA 120

Qy 121 GGGAAATCTCTCAGCTCCCTGATTTATGCTGCCACCAACTTGGCAGATGGGTTCCCATCA 180  
Db 121 GGGAAATCTCTCAGCTCCCTGATTTATGCTGCCACCAACTTGGCAGATGGGTTCCCATCA 180

Qy 181 AGTTTCAGTGGCAGTGGATCTGGCACAATAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240  
Db 181 AGTTTCAGTGGCAGTGGATCTGGCACAATAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240

Qy 241 GAAGATTTTGTAAATTTATTTACTGTCTCAACAAGTTTACAGTTCTCCATTCAGTTCCGTTGCT 300  
Db 241 GAAGATTTTGTAAATTTATTTACTGTCTCAACAAGTTTACAGTTCTCCATTCAGTTCCGTTGCT 300

Qy 301 GGGACCAAGCTGGAGCTGAAA 321  
Db 301 GGGACCAAGCTGGAGCTGAAA 321

RESULT 4  
US-10-310-113-1  
; Sequence 1, Application US/10310113  
; Publication No. US20030176664A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; APPLICANT: WONG, HING C.  
; APPLICANT: NIEVES, ESPERANZA LILIANA  
; APPLICANT: MOSQUERA, LUIS A.  
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING  
; FILE REFERENCE: 58122(71758)  
; CURRENT APPLICATION NUMBER: US/10/310,113  
; CURRENT FILING DATE: 2002-12-04  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/343,306  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: 08/814,806  
; PRIOR FILING DATE: 1997-03-10  
; NUMBER OF SEQ ID NOS: 169  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Murine sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(321)  
US-10-310-113-1

Query Match 100.0%; Score 321; DB 6; Length 321;  
Best Local Similarity 100.0%; Pred. No. 7e-94;  
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCAATCTCTGGGAGAAAGTGTCAACC 60  
Db 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCAATCTCTGGGAGAAAGTGTCAACC 60

Qy 61 ATCATATGCTGCGCAAGTCAGACCATTTGATGATACATGTTAGCATGGTATCAGCAGAAACCA 120  
Db 61 ATCATATGCTGCGCAAGTCAGACCATTTGATGATACATGTTAGCATGGTATCAGCAGAAACCA 120

Qy 121 GGGAAATCTCTCAGCTCCCTGATTTATGCTGCCACCAACTTGGCAGATGGGTTCCCATCA 180  
Db 121 GGGAAATCTCTCAGCTCCCTGATTTATGCTGCCACCAACTTGGCAGATGGGTTCCCATCA 180

Qy 181 AGTTTCAGTGGCAGTGGATCTGGCACAATAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240  
Db 181 AGTTTCAGTGGCAGTGGATCTGGCACAATAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240

Qy 241 GAAGATTTTGTAAATTTATTTACTGTCTCAACAAGTTTACAGTTCTCCATTCAGTTCCGTTGCT 300  
Db 241 GAAGATTTTGTAAATTTATTTACTGTCTCAACAAGTTTACAGTTCTCCATTCAGTTCCGTTGCT 300

Qy 301 GGGACCAAGCTGGAGCTGAAA 321  
Db 301 GGGACCAAGCTGGAGCTGAAA 321

RESULT 5  
US-10-230-880-1  
; Sequence 1, Application US/10230880  
; Publication No. US20030190705A1  
; GENERAL INFORMATION:  
; APPLICANT: WONG, HING C.  
; APPLICANT: STINSON, JEFFREY L.  
; APPLICANT: MOSQUERA, LUIS A.  
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES  
; FILE REFERENCE: 71758/58066  
; CURRENT APPLICATION NUMBER: US/10/230,880  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: 09/990,586  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/343,306  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(321)  
US-10-230-880-1

Query Match 100.0%; Score 321; DB 6; Length 321;  
Best Local Similarity 100.0%; Pred. No. 7e-94;  
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCAATCTCTGGGAGAAAGTGTCAACC 60  
Db 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCAATCTCTGGGAGAAAGTGTCAACC 60

Qy 61 ATCATATGCTGCGCAAGTCAGACCATTTGATGATACATGTTAGCATGGTATCAGCAGAAACCA 120  
Db 61 ATCATATGCTGCGCAAGTCAGACCATTTGATGATACATGTTAGCATGGTATCAGCAGAAACCA 120

Qy 121 GGGAAATCTCTCAGCTCCCTGATTTATGCTGCCACCAACTTGGCAGATGGGTTCCCATCA 180  
Db 121 GGGAAATCTCTCAGCTCCCTGATTTATGCTGCCACCAACTTGGCAGATGGGTTCCCATCA 180

Qy 181 AGTTTCAGTGGCAGTGGATCTGGCACAATAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240  
Db 181 AGTTTCAGTGGCAGTGGATCTGGCACAATAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240

Qy 241 GAAGATTTTGTAAATTTATTTACTGTCTCAACAAGTTTACAGTTCTCCATTCAGTTCCGTTGCT 300  
Db 241 GAAGATTTTGTAAATTTATTTACTGTCTCAACAAGTTTACAGTTCTCCATTCAGTTCCGTTGCT 300

Qy 301 GGGACCAAGCTGGAGCTGAAA 321  
Db 301 GGGACCAAGCTGGAGCTGAAA 321











; OTHER INFORMATION: construct of DNA encoding bispecific single chain  
; OTHER INFORMATION: antibody comprising anti-zeta-chain/anti-EpCAM  
; OTHER INFORMATION: domains.  
US-11-036-098-17

```
Query Match          73.6%; Score 236.2; DB 10; Length 1637;
Best Local Similarity 83.5%; Pred. No. 5.9e-66;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy 1 GACATTCAGATGACCCAGTCTCTGCTCCAGTCTGCATCTCTGGGAGAAAGTGTACCC 60
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 67 GATATCCAGATGACACAGTCTCTGCTCCCTGCTGCTGCCGCCGAGAGAAATTGTACG 126
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 61 ATCAGATGCTTGGCAAGTCAGACCATTTGATACATAGTTAGCATGGTATCAGCAGAAACCA 120
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 127 ATCAGATGCTTGGCAAGTCAGACCATTTGATACATAGTTAGCATGGTATCAGCAGAAACCA 186
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 121 GGGAAATCTCTCAGCTCTCTGATTTATGCTGGCCACCACTTGGCAGATGGGGTCCCATCA 180
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 187 GGGAAATCTCTCAGCTCTCTGATCTATAGTGCAACCCAGCTTGGCAGCGGATCCCATCA 246
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 181 AGGTTTCAGTGGCAGTGGATCTGGCACAATAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 247 AGGTTTCAGCGGAGTAGATCTGGTACACAGTATTTCTTTAAGATCAGCAGACTACAGGTT 306
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 241 GAAGATTTTGTAAATTTATTACTGTCAACAAGTTTACAGTTTCTCCATTTCAGTTTCGTTGCT 300
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 307 GAAGATCTGGAAATCTATTACTGTCTACAGCGTTATAGTAATCCCAACAGTTTGGAGCT 366
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 301 GGGACCAAGCTGGAGCTGAAA 321
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 367 GGGACCAAGCTGGAGCTGAAA 387
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: April 18, 2006, 22:26:16  
Job time : 575 secs

GenCore version 5.1.7  
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QM nucleic - nucleic search, using sw model

Run on: April 18, 2006, 18:31:21 ; Search time 1340 Seconds  
(without alignments)  
964.876 Million cell updates/sec

Title: US-10-764-140-1

Perfect score: 321

Sequence: 1 gacattcagatgaccagtc.....ggaccaagctgagtgtaa 321

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9281099 seqs, 2013915447 residues

Total number of hits satisfying chosen parameters: 18562198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.New.\*

- 1: /SIDSS/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 2: /SIDSS/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /SIDSS/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /SIDSS/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 5: /SIDSS/ptodata/2/pubpna/US03\_NEW\_PUB.seq.\*
- 6: /SIDSS/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 7: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 8: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 9: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 10: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 11: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 12: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 13: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 14: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 15: /SIDSS/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	321	100.0	321	11	US-11-122-622-1
2	321	100.0	321	14	US-11-087-528-1
3	240.2	74.8	411	14	US-11-136-527-190
4	240.2	74.8	411	14	US-11-136-527-4286
5	226.6	70.6	714	14	US-11-128-900-62
6	226.6	70.6	13281	9	US-10-893-483-188
7	224.6	70.0	322	12	US-11-144-248-54
8	224.6	70.0	322	14	US-11-144-248-54
9	224.6	70.0	322	14	US-11-182-343-54
10	221.8	69.1	708	14	US-11-086-289-7
11	221.8	69.1	13281	9	US-10-893-483-188
12	220.2	68.6	324	11	US-11-193-739-173
13	220.2	68.6	324	14	US-11-049-536-173
14	218.6	68.1	322	7	US-10-956-008-75
15	218.6	68.1	324	11	US-11-193-739-241
16	218.6	68.1	324	14	US-11-049-536-241
17	218	67.9	326	12	US-11-144-248-53
18	218	67.9	326	14	US-11-144-248-53

19	218	67.9	326	14	US-11-182-343-53	Sequence 53, Appl
20	217	67.6	12233	9	US-10-893-483-187	Sequence 187, App
c 21	217	67.6	12233	9	US-10-893-483-187	Sequence 187, App
22	215.4	67.1	315	14	US-11-155-775-51	Sequence 51, Appl
23	215.4	67.1	321	14	US-11-084-554-5	Sequence 5, Appl
24	215.4	67.1	321	14	US-11-136-250-5	Sequence 5, Appl
25	215.4	67.1	324	11	US-11-193-739-453	Sequence 453, App
26	215.4	67.1	324	11	US-11-193-739-597	Sequence 597, App
27	215.4	67.1	324	14	US-11-049-536-453	Sequence 597, App
28	215.4	67.1	324	14	US-11-049-536-597	Sequence 597, App
29	215.4	67.1	357	9	US-10-993-543-121	Sequence 121, App
30	215.4	67.1	1721	9	US-10-988-207-27	Sequence 27, Appl
31	213.8	66.6	315	14	US-11-155-775-55	Sequence 55, Appl
32	213.8	66.6	321	14	US-11-051-453-37	Sequence 37, Appl
33	213.8	66.6	322	12	US-11-144-248-13	Sequence 13, Appl
34	213.8	66.6	322	14	US-11-144-222-13	Sequence 13, Appl
35	213.8	66.6	322	14	US-11-182-343-13	Sequence 13, Appl
36	213.8	66.6	324	11	US-11-193-739-481	Sequence 481, App
37	213.8	66.6	324	14	US-11-049-536-481	Sequence 481, App
38	213.8	66.6	388	14	US-11-009-840A-206	Sequence 206, App
39	213.8	66.6	388	14	US-11-009-873A-206	Sequence 206, App
40	213.8	66.6	388	14	US-11-009-769A-206	Sequence 206, App
41	213.8	66.6	708	14	US-11-086-289-3	Sequence 3, Appl
42	213.8	66.6	708	14	US-11-086-289-19	Sequence 19, Appl
43	212.2	66.1	308	11	US-11-193-739-21	Sequence 21, Appl
44	212.2	66.1	308	14	US-11-049-536-21	Sequence 21, Appl
45	212.2	66.1	321	8	US-10-850-635-17	Sequence 17, Appl

#### ALIGNMENTS

##### RESULT 1

US-11-122-622-1  
; Sequence 1, Application US/11122622  
; Publication No. US20060039901A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
; TITLE OF INVENTION: OF USE THEREOF  
; FILE REFERENCE: 71758/46943-CIP2  
; CURRENT APPLICATION NUMBER: US/11/122,622  
; PRIOR FILING DATE: 2005-05-05  
; PRIOR APPLICATION NUMBER: US/09/990,586  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(321)  
US-11-122-622-1

Query Match	100.0%;	Score 321;	DB 11;	Length 321;
Best Local Similarity	100.0%;	Pred. No. 2.4e-92;		
Matches 321;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GACATTCAGATGACCCAGTCTCCTCCCTCCAGTCTGCATCTCTGGGAGAAAGTGTCA	60	
Db	1	GACATTCAGATGACCCAGTCTCCTCCCTCCAGTCTGCATCTCTGGGAGAAAGTGTCA	60	
QY	61	ATCACATGCTGGCAAGTCAGACCATTTGATACATGTTAGCATGTTATCAGCAGAAACCA	120	
Db	61	ATCACATGCTGGCAAGTCAGACCATTTGATACATGTTAGCATGTTATCAGCAGAAACCA	120	
QY	121	GGGAATCTCTCAGCTCCTGATTTATGCTGCCACCACTTGGCAGATGGGTCCCATCA	180	

Db	121	GGGAAATCTCTCAGCTCCTGATTTATGCTGCCACCAACTGGGCGAGATGGGGTCCCATCA	180
Qy	181	AGGTTTCAGTGGCAGTGGATCTGGCAAAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT	240
Db	181	AGGTTTCAGTGGCAGTGGATCTGGCAAAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT	240
Qy	241	GAAGATTTTGTAAATATTACTGTCAACAAGTTTACAGTTCTTCCATTACGTTCCGGTGCT	300
Db	241	GAAGATTTTGTAAATATTACTGTCAACAAGTTTACAGTTCTTCCATTACGTTCCGGTGCT	300
Qy	301	GGGACCAAGCTGGAGCTGAAA	321
Db	301	GGGACCAAGCTGGAGCTGAAA	321

## RESULT 2

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US-11-087-528-1
; Sequence 1, Application US/11087528
; Publication No. US20050271664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; APPLICANT: WEN, JING HAI
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: TNA-005.06
; CURRENT APPLICATION NUMBER: US/11/087,528
; PRIOR FILING DATE: 2005-03-22
; PRIOR APPLICATION NUMBER: 10/293,417
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ..(321)
US-11-087-528-1

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### RESULT 3

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US-11-136-527-190
; Sequence 190, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 190
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-190

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## RESULT 4

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US-11-136-527-4286
; Sequence 4286, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4286
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-4286
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Best Local Similarity		82.2%;	Pred. NO. 1.9e-66;
Matches		264;	Conservative 18; Mismatches 36; Indels 3; Gaps 1
Qy	1	GACATTCAGATGACCCAGTCTCCCTGCGCTCCAGAGTCGATCTCTGGGAGAAAGTGTCA	60
Db	85	GACATCCATGTGACACAGTCTCTGCGCTCCCTGTCTGTCATCTCGGAAGAAATTTC	144
Qy	61	ATCACATGCTCTGGCAAGTCAGACCAATGATACATGTTAGCATGGTATCAGCAGAAACCA	120
Db	145	ATCACATGCCAGGCAAGCCAGGACATGGKARTTSGTTATYATGGTATCAGCAGNAACCA	204
Qy	121	GGGAAATCTCTCAGTCTCTGAGTCTCTGATTTATGCTGCCACCACTTTGGCAGATGGGGTCCCATCA	180
Db	205	GGGAAATCTCTCAGTCTCTGATCTATATGTGCAACCAKCTTGGCAGATGGGGTCCCATCA	264
Qy	181	AGGTTCAGTGGCAGTGGATCTGGCAACAAATTTCTTTCAAGATCAGCAGCCTACAGGCT	240
Db	265	AGGTTCAGYGGCAGTAGATCTGGCACACAGTATTTCTCTTAAGATCAGCAGAGTACRGGTT	324
Qy	241	GAAGATTTTGTAAATTTACTGTCAACAGTTTTACAGTTCTCCATTCACGTTGGTGCT	300
Db	325	GAAGATATTGGAAYCTATTACTGTCTACAGKYTTMTAGTKCTC---TSACGTTGGTGSW	381
Qy	301	GGGACCAAGCTGGAGCTGAA	321
Db	382	GGSACCAAGCTGGARWTSAA	402

RESULT 5  
 US-11-128-900-62  
 ; Sequence 62, Application US/11128900  
 ; Publication No. US20050287136A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HANSON, DOUGLAS C.  
 ; APPLICANT: NEVEU, MARK J.  
 ; APPLICANT: MOELLER, EILEEN E.  
 ; APPLICANT: HANKE, JEFFREY H.  
 ; APPLICANT: GILMAN, STEVEN C.  
 ; APPLICANT: DAVIS, C. GEOFFREY  
 ; APPLICANT: CORVALAN, JOSE R.  
 ; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
 ; FILE REFERENCE: ABX-PFI DIV3  
 ; CURRENT APPLICATION NUMBER: US/11/128,900  
 ; CURRENT FILING DATE: 2005-05-12  
 ; PRIOR APPLICATION NUMBER: US 10/776649  
 ; PRIOR FILING DATE: 2004-02-10  
 ; PRIOR APPLICATION NUMBER: US 10/613497  
 ; PRIOR APPLICATION NUMBER: 2003-07-01  
 ; PRIOR APPLICATION NUMBER: US 09/472087  
 ; PRIOR FILING DATE: 1999-12-23  
 ; PRIOR APPLICATION NUMBER: US 60/113647  
 ; PRIOR FILING DATE: 1998-12-23  
 ; NUMBER OF SEQ ID NOS: 147  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 62  
 ; LENGTH: 714  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-11-128-900-62

Query Match	70.6%	Score	226.6	DB	14	Length	714
Best Local Similarity	81.6%	Pred.	No. 5.5e-62				
Matches	262	Conservative	0	Mismatches	59	Indels	0
Gaps	0						

  

QY	1	GACATTCAGATGACCCAGTCTCTCGCTCCAGTCTGCATCTCTGGGAGAAAGTGTCA	60
DB	67	GACATTCAGATGACCCAGTCTCTCGCTCCAGTCTGCATCTCTGGGAGAGACAGAGTCA	126
QY	61	ATCACATCGCTGGCAAGTCAGACCATTCATGATCGTTAGCATGGTTACAGCAAGAACCA	120
DB	127	ATCACTTCGGGGCAAGTCAGAGCATTAACAGCTATTATTGATTGGTATCAGCAAGAACCA	186
QY	121	GGGAAATCTCCTCAGCTCCTGATTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA	180

Accession	Position	Sequence	Length
Db	187	GGGAAAGCCCTAAACTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA	246
Qy	181	AGGTTCAAGTGGCAGTGGATCTGGCACAAAATTTTCTTTCAAGATCAGACGCTACAGGCT	240
Db	247	AGGTTCAAGTGGCAGTGGATCTGGACACAGATTTCACTCTCCACATCAGCAGTCTGCAACCT	306
Qy	241	GAAGATTTTGTAAATTATTAAGTGTCAACAAGTTTACAGTTCTCCATTCAAGTTCGGTGCT	300
Db	307	GAAGATTTTGCAACTTACTACTGTCAACAGTATTTACAGTACTCCATTCACTTTCGGGCCCT	366
Qy	301	GGGACCAAGCTGGAGCTGAAA	321
Db	367	GGGACCAAAAGTGGAAATCAAA	387

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RESULT 6
US-10-893-483-188/c
; Sequence 188, Application US/10893483
; Publication No. US20060026696A1
; GENERAL INFORMATION:
; APPLICANT: Buelow, Roland
; APPLICANT: Platzzer, Josef
; APPLICANT: Schooten, Wim van
; TITLE OF INVENTION: Humanized Immunoglobulin Loci
; FILE REFERENCE: 39691-0807A
; CURRENT APPLICATION NUMBER: US/10/893,483
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: 60/487,733
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 188
; LENGTH: 13281
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain locus
US-10-893-483-188

```

Query Match	70.8%	Score	226.6	DB	9	Length	13281
Best Local Similarity	81.6%	Pred. No.	2.1e-61				
Matches	262	Conservative	0	Mismatches	59	Indels	0
Qy	1	GACATTCAGATGACCCAGTCTCTCGCTCCAGTCTCCAGTCTGCACTCTCGGAGAAAGTGTCACC	60				
Db	9439	GACATCCAGATGACCCAGTCTCTCTCCACCTCTGTCATCTGTAGGAGACAGAGTCACC	9380				
Qy	61	ATCACATGCTGCGCAAGTCAGACATTTGATACATGTTAGCATGGTTAGCATGGTATCAGCAGAAACCA	120				
Db	9379	ATCACATGCGCGGCCAGTCAGAGTATTAGTAGCTGGCTGGTATCAGCAGAAACCA	9320				
Qy	121	GGGAAATCTCTCAGCTCTCGATTTATGTCGCCACCAATTTGGCAGATGGGGTCCCATCA	180				
Db	9319	GGGAAAGCCCTAAGCTCTGATCTATGATGCTCCAGTTTGGAAAGTGGGGTCCCATCA	9260				
Qy	181	AGSTTCAGTGGCAGTGGATCTGSCACAAAATTTCTTTCAAGATCAGCAGCTTACAGGCT	240				
Db	9259	AGSTTCAGCGGCAGTGGATCTGGGACAGAAATTCACCTCTCACCATCAGCAGCTTGCAGCCT	9200				
Qy	241	GAAGATTTTGTAAATTTACTGTCTCAACAAAGTTTACAGTTTCTCCATTCAGTTTCGGTGTCT	300				
Db	9199	GATGATTTTGTCACTTTACTTGCCAAACAGTATAATAGTATTATCTCTCACTTTTCGGCGGT	9140				
Qy	301	GGGACCAAGCTGGAGCTGAAA	321				
Db	9139	GGGACCAAGCTGGATCTCAAA	9119				

RESULT 7  
US-11-144-248-54  
; Sequence 54, Application US/11144248  
: Publication No. US20050244408A1



Qy	61	ATCATGCTGGCGAAGTCAGACCAATTGATCATGGTTAGCATGTGTTATCAGCAGAAACCA	120
Db	61	ATCACTTCGGGGCAAGTCAGACCAATTGATCATGGTTAGCATGTGTTATCAGCAGAAACCA	120
Qy	121	GGGAAATCTCTCAGCTCTGATTTATGCTGCCACCAACTTCGCGAGATGGGTCCCATCA	180
Db	121	GGGAAAGCCCCCTAECTCTGATCATGTCATCCAGTTTTCAGAGTGGGTCCCATCA	180
Qy	181	AGTTTCAGTCGGCAGTGGATCTGGCCAAAAATTTCTTTCAAGATCAGCAGCCTACAGGT	240
Db	181	AGTTTCAGTCGGCAGTGGATCTGGGCAGATTTCACTCTCACCATCAGCAGTCTGCAACCT	240
Qy	241	GAAGATTTTGTAAATTAATTACTGTCAACAAGTTTACAGTTCTTCCATTACAGTTTCGGTGCT	300
Db	241	GAAGATTTTGCACCTTACTACTGTCAACAGATTTACATRCCCAATYCHCTTTGCGCGA	300
Qy	301	GGGACCAAGCTGGAGCTGAAA	321
Db	301	GGGACCAAGCTGGAGCTCAAA	321

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RESULT 10
US-11-086-289-7
; Sequence 7, Application US/11086289
; Publication No. US2006002929A1
; GENERAL INFORMATION:
; APPLICANT: KHARE, SANJAY D.
; APPLICANT: KELLERMANN, SIRID-AIMEE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; FILE REFERENCE: 06843.0094-00000
; CURRENT APPLICATION NUMBER: US/11/086,289
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 60/555,396
; PRIOR FILING DATE: 2004-03-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 7
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-086-289-7

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## RESULT 11

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US-10-893-483-188
; Sequence 188, Application US/10893483
; Publication No. US20060026696A1
; GENERAL INFORMATION:
; APPLICANT: Buelow, Roland
; APPLICANT: Platzer, Josef
; APPLICANT: Schooten, Wim van
; TITLE OF INVENTION: Humanized Immunoglobulin Loci
; FILE REFERENCE: 39691-0007A
; CURRENT APPLICATION NUMBER: US/10/893,483
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: 60/487,733
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 188
; LENGTH: 13281
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain locus
US-10-893-483-188

Query Match          69.1%; Score 221.8; DB 9; Length 13281;
Best Local Similarity 80.7%; Pred. No. 7.3e-60;
Matches 259; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy      1  GACATTCAGATGACCCAGTCTCTCGCTCCCAAGTCTGCAATCTCTGGGAGAAAGTGTCAAC 60
Db      12395 GACATTCAGATGACCCAGTCTCCATCTCCCTCTGCAATCTGTAGGAGACAGAGTCAAC 12454

Qy      61  ATCATGTCCTGGCAAGTCAGACCAATGATACATGTTAGCATGTTATCAGCAGAAACCA 120
Db      12455 ATCACTTGC CGGCAAGTCAGAGCAATTAGCAGTATTTAAATTGGTATCAGCAGAAACCA 12514

Qy      121 GGGAAATCTCTCAGCTCTCATTTATGCTGCCAACAATTTGGCAGATGGGGTCCCATCA 180
Db      12515 GGGAAAGCCCCTAAGCTCTCATCTATGTCATGTCGCAAGTTTGC AAAAGTGGGGTCCCATCA 12574

Qy      181 AGGTTTCAGTGGCAGTGGATCTGGCAAAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT 240
Db      12575 AGGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 12634

Qy      241 GAAGATTTTGTAAATTTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTTCGGTGTCT 300
Db      12635 GAAGATTTTGC AACTTACTCTGTCTCAACAGAGTTACAGTACCCTCTCACTTTCGGCGGA 12694

Qy      301 GGGACCAAGCTGGAGCTGAAA 321
Db      12695 GGGACCAAGGTGGAGATTAAA 12715

RESULT 12
US-11-199-739-173
; Sequence 173, Application US/11199739
; Publication No. US20060057138A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive R.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Pieters, Henk
; APPLICANT: Hoet, Rene
; APPLICANT: Hufton, Simon E.
; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
; FILE REFERENCE: 10280-135001
; CURRENT APPLICATION NUMBER: US/11/199,739
; CURRENT FILING DATE: 2005-08-09
; PRIOR APPLICATION NUMBER: US 11/049,536
; PRIOR FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US 10/916,840
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 726

```







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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2006, 13:32:40 ; Search time 230 Seconds  
(without alignments)  
358.899 Million cell updates/sec

Title: US-10-764-140-4  
Perfect score: 617  
Sequence: 1 ETQLQSGFELVKPGASVQV.....RDVTTALDFWQGTTLTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.\*

1: uniprot\_prot.\*

2: uniprot\_trembl.\*

\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	476.5	77.2	481	2 Q8VCV5_MOUSE	Q8VCV5 mus musculus
2	475	77.0	117	2 Q9QXF0_MOUSE	Q9QXF0 mus musculus
3	474	76.8	117	2 Q9QXE9_MOUSE	Q9QXE9 mus musculus
4	470	76.2	134	2 Q65ZR6_MOUSE	Q65ZR6 mus musculus
5	470	76.2	483	2 Q4VAB6_MOUSE	Q4VAB6 mus musculus
6	463	75.0	117	1 HV12_MOUSE	P01756 mus musculus
7	460	74.6	117	1 HV13_MOUSE	P01757 mus musculus
8	447	72.4	470	2 Q7TMM1_MOUSE	Q7TMM1 mus musculus
9	442.5	71.7	488	2 Q91WR1_MOUSE	Q91WR1 mus musculus
10	442	71.6	472	2 Q6PUA7_MOUSE	Q6PUA7 mus musculus
11	439	71.2	123	2 Q8VJL1_MOUSE	Q8VJL1 mus musculus
12	433.5	70.3	118	1 HV51_MOUSE	P06330 mus musculus
13	425	68.9	120	2 Q920E8_MOUSE	Q920E8 mus musculus
14	420.5	68.2	485	2 Q58E61_MOUSE	Q58E61 mus musculus
15	420	68.1	458	2 Q5BJZ2_RAT	Q5BJZ2 rattus norv
16	419	67.9	117	1 HV14_MOUSE	P01758 mus musculus
17	418	67.7	136	1 HV15_MOUSE	P01759 mus musculus
18	418	67.1	120	1 HV03_MOUSE	P01747 mus musculus
19	412	66.8	477	2 Q58E56_MOUSE	Q58E56 mus musculus
20	411	66.6	481	2 Q91WT1_MOUSE	Q91WT1 mus musculus
21	410	66.5	142	2 Q924Q1_MOUSE	Q924Q1 mus musculus
22	408	66.1	170	2 Q925S2_MOUSE	Q925S2 mus musculus
23	407.5	66.0	145	2 Q924Q9_MOUSE	Q924Q9 mus musculus
24	404.5	65.6	143	2 Q924R0_MOUSE	Q924R0 mus musculus
25	404.5	65.6	145	2 Q924R4_MOUSE	Q924R4 mus musculus
26	402.5	65.2	145	2 Q924Q6_MOUSE	Q924Q6 mus musculus
27	402	65.2	146	2 Q924Q8_MOUSE	Q924Q8 mus musculus
28	401.5	65.1	141	2 Q924Q4_MOUSE	Q924Q4 mus musculus
29	400.5	64.9	137	2 Q924R6_MOUSE	Q924R6 mus musculus
30	400	64.8	140	1 HV02_MOUSE	P01746 mus musculus
31	400	64.8	146	2 Q924Q3_MOUSE	Q924Q3 mus musculus

32	399.5	64.7	243	2 Q7TQM2_MOUSE	Q7TQM2 mus musculus
33	399.5	64.7	465	2 Q6PUB2_MOUSE	Q6PUB2 mus musculus
34	399	64.7	146	2 Q924R8_MOUSE	Q924R8 mus musculus
35	398.5	64.6	139	1 HV07_MOUSE	P01751 mus musculus
36	398.5	64.6	145	2 Q924Q7_MOUSE	Q924Q7 mus musculus
37	398.5	64.6	590	2 Q4V9V8_MOUSE	Q4V9V8 mus musculus
38	398.5	64.6	617	2 Q4KML5_MOUSE	Q4KML5 mus musculus
39	398	64.5	468	2 Q56W9_MOUSE	Q56W9 mus musculus
40	397.5	64.4	145	2 Q924R1_MOUSE	Q924R1 mus musculus
41	397	64.3	458	2 Q5BK05_RAT	Q5BK05 rattus norv
42	396.5	64.3	109	2 Q8K172_MOUSE	Q8K172 mus musculus
43	395.5	64.1	482	2 Q9JL75_MOUSE	Q9JL75 mus musculus
44	394.5	63.9	143	2 Q924P9_MOUSE	Q924P9 mus musculus
45	394	63.9	140	2 Q924P8_MOUSE	Q924P8 mus musculus

#### ALIGNMENTS

RESULT 1  
Q8VCV5\_MOUSE  
ID Q8VCV5\_MOUSE PRELIMINARY; PRT; 481 AA.  
AC Q8VCV5\_  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DE LOC238447 protein.  
GN Names=LOC238447;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Mix FVB/N;  
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603999;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,  
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grummond J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Mix FVB/N;  
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
RG NIH MGC Project;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC018455; AAH18455.1; -; mRNA.  
DR HSSP; P01810; 2FBU.  
DR SMR; Q8VCV5; 20-239.  
DR Ensemble; ENSMUSG00000021155; Mus musculus.  
DR GO; GO:0003823; F:antigen binding; IEA.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.

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DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ Immunoglobulin domain.
KW SEQUENCE 481 AA; 52326 MW; 52B44C5826807143 CRC64;

Query Match 77.2%; Score 476.5; DB 2; Length 481;
Best Local Similarity 75.4%; Pred. No. 4.1e-39;
Matches 89; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 1 EIQLOQSGPELVKPGASVQVSKTXGYSFTDYNVYVRQSHGKSLWIGYIDPYNGITTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EIQLOQSGPELVKPGTSVKVSKASCYSFIDYNIYVWKQSHGKSLWIGYIDPYNGSSY 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 DONFGKATLTVDKSTTAFMHLNSLTSDSAVYFCARDVTTA-LDPWQGGTTLTVSS 117
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NQKFGKATLTVDKSSNTAFMHLNSLTSDSAFYCAREWYGAWFAWQGGTTLTVSSA 137
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 2
ID Q9QXF0_MOUSE PRELIMINARY; PRT; 117 AA.
AC Q9QXF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA *Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=249887;
RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT "Two murine natural polyreactive autoantibodies are encoded by
RT nonmutated germ-line genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
DR EMBL; AJ225174; CAB65237.1; -; mRNA.
DR PIR; F33932; F33932.
DR HSP; P01751; INQB.
DR SMR; Q9QXE9; 1-117.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match 76.8%; Score 474; DB 2; Length 117;
Best Local Similarity 75.2%; Pred. No. 1.5e-39;
Matches 88; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 1 EIQLOQSGPELVKPGASVQVSKTXGYSFTDYNVYVRQSHGKSLWIGYIDPYNGITTY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVOLQSGPELVKPGASVKMSCKASGYTFTDYMKVWKQSHGKSLWIGDINPNNGGTSY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 DONFGKATLTVDKSTTAFMHLNSLTSDSAVYFCARDVTTALDFWQGGTTLTVSS 117
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NQKFGKATLTVDKSSSTAYMQLNSLTSDSAVYCYARDYAMDYWGQGTSTVTVSS 117
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
ID Q85ZR6_MOUSE PRELIMINARY; PRT; 134 AA.
AC Q85ZR6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Ab 126.33 heavy chain variable and joining regions (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=91237115; PubMed=1709665;
RA Rueff-Juy D., Marche P.N., Drapier A.-M., Cazenave P.-A.;
RT "Junctional diversity of H and L chains allows the coexpression of two
RT mutually exclusive idiotopes (Id1104 and Id1558).";
RL J. Immunol. 146:4024-4030(1991).
DR EMBL; M74139; AAA37776.1; -; mRNA.
DR SMR; Q652R6; 18-134.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.

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FT NON TER 1 1
SQ SEQUENCE 134 AA; 14908 MW; 1852D86D26FC7567 CRC64;

Query Match
Best Local Similarity 76.2%; Score 470; DB 2; Length 134;
Matches 88; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 1 EIQLOQSGPELVKPGASVQVCKTXGYSFTDYNVYWRQSHGKSLWIGYIDPNYNGITY 60
DB 18 EVQLQSGPELVKPGASVQVCKTXGYSFTDYNVYWRQSHGKSLWIGYIDPNYNGITY 77
QY 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDSVAVFCARDVTTLDFWQGGTTLTVSS 117
DB 78 NQKFKGKATLTVDKSSSTAYMQLNSLTSDSVAVYCARDYVDFYDWGQGGTTLTVSS 134

RESULT 5
Q4VAB6_MOUSE
ID Q4VAB6_MOUSE PRELIMINARY; PRT; 483 AA.
AC Q4VAB6_MOUSE STANDARD; PRT; 117 AA.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN NCBI_TaxID=10090;
RP PROTEIN SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RL Biochemistry 21:5415-5424(1982).
CC -!- MISCELLANEOUS: The sequence of the light chain of this IgM myeloma
CC protein has also been determined.
CC -!- MISCELLANEOUS: This protein binds dextran.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR: A02039; MHMS48.
DR HSSP; P01751; INQB.
DR SMR; P01756; 1-117.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 116 Ig-like.
FT CARBOHYD 55 55 N-linked (GlcNAc...) (complex).
FT DISULFID 22 96 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF9ACE4BB447E41 CRC64;

Query Match
Best Local Similarity 75.0%; Score 463; DB 1; Length 117;
Matches 87; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 EIQLOQSGPELVKPGASVQVCKTXGYSFTDYNVYWRQSHGKSLWIGYIDPNYNGITY 60
DB 1 EVQLQSGPELVKPGASVQVCKTXGYSFTDYNVYWRQSHGKSLWIGYIDPNYNGITY 60
QY 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDSVAVFCARDVTTLDFWQGGTTLTVSS 117
DB 61 NQKFKGKATLTVDKSSSTAYMQLNSLTSDSVAVYCARDYVDFYDWGQGGTTLTVSS 117

RESULT 7
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC HV13_MOUSE STANDARD; PRT; 117 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig heavy chain V region J558.
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

```

```

FT NON TER 1 1
SQ SEQUENCE 134 AA; 14908 MW; 1852D86D26FC7567 CRC64;

Query Match
Best Local Similarity 75.2%; Score 470; DB 2; Length 134;
Matches 88; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 1 EIQLOQSGPELVKPGASVQVCKTXGYSFTDYNVYWRQSHGKSLWIGYIDPNYNGITY 60
DB 18 EVQLQSGPELVKPGASVQVCKTXGYSFTDYNVYWRQSHGKSLWIGYIDPNYNGITY 77
QY 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDSVAVFCARDVTTLDFWQGGTTLTVSS 117
DB 78 NQKFKGKATLTVDKSSSTAYMQLNSLTSDSVAVYCARDYVDFYDWGQGGTTLTVSS 134

RESULT 5
Q4VAB6_MOUSE
ID Q4VAB6_MOUSE PRELIMINARY; PRT; 483 AA.
AC Q4VAB6_MOUSE STANDARD; PRT; 483 AA.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN NCBI_TaxID=10090;
RP PROTEIN SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RL Biochemistry 21:5415-5424(1982).
CC -!- MISCELLANEOUS: The sequence of the light chain of this IgM myeloma
CC protein has also been determined.
CC -!- MISCELLANEOUS: This protein binds dextran.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR: A02039; MHMS48.
DR HSSP; P01751; INQB.
DR SMR; P01756; 1-117.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 116 Ig-like.
FT CARBOHYD 55 55 N-linked (GlcNAc...) (complex).
FT DISULFID 22 96 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF9ACE4BB447E41 CRC64;

Query Match
Best Local Similarity 75.0%; Score 463; DB 1; Length 117;
Matches 87; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 EIQLOQSGPELVKPGASVQVCKTXGYSFTDYNVYWRQSHGKSLWIGYIDPNYNGITY 60
DB 1 EVQLQSGPELVKPGASVQVCKTXGYSFTDYNVYWRQSHGKSLWIGYIDPNYNGITY 60
QY 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDSVAVFCARDVTTLDFWQGGTTLTVSS 117
DB 61 NQKFKGKATLTVDKSSSTAYMQLNSLTSDSVAVYCARDYVDFYDWGQGGTTLTVSS 117

RESULT 7
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC HV13_MOUSE STANDARD; PRT; 117 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig heavy chain V region J558.
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

```

OC Muroidea; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=80078170; PubMed=6765983;  
 RA Schilling J., Clevinger B., Davie J.M., Hood L.;  
 RT "Amino acid sequence of homogeneous antibodies to dextran and DNA  
 rearrangements in heavy chain V-region gene segments.";  
 RL Nature 283:35-40(1980).  
 CC -1- MISCELLANEOUS: The sequences of 10 hybridoma proteins that also  
 bind dextran differ from that shown at 1-7 positions, many of  
 which occur in the D and J segments.  
 CC -1- MISCELLANEOUS: This protein binds dextran.  
 CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC -----  
 DR PIR; A26242; MHMSJ5.  
 DR HSP; P01751; INQB.  
 DR SMR; P01757; 1-117.  
 DR InterPro; IPR007110; Ig-like.  
 DR SMART; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin domain;  
 Immunoglobulin v region.  
 FT DOMAIN 1 116 Ig-like.  
 FT DISULFID 22 96 By similarity.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 13025 MW; 292E2AF4B8447E41 CRC64;  
 Query Match 74.6%; Score 460; DB 1; Length 117;  
 Best Local Similarity 74.4%; Pred. No. 3.8e-38;  
 Matches 87; Conservative 13; Mismatches 17; Indels 0; Gaps 0;  
 QY 1 EIQLOQSGPELVKPGASVOVSKCTGYSTFYNNVYVWQSHGKSLWIGYIDPYNGITY 60  
 Db 1 EIQLOQSGPELVKPGASVOVSKCTGYSTFYNNVYVWQSHGKSLWIGYIDPYNGITY 60  
 QY 61 DQNFKGKATLVKSKSTTAFMHLNSLSDSDSAVYFCARDVTVTALDFWGGTTLTVSS 117  
 Db 61 NQKFGKATLVKSKSTTAFMHLNSLSDSDSAVYFCARDVTVTALDFWGGTTLTVSS 117  
 RESULT 8  
 O7TMK1 MOUSE  
 ID Q7TMK1 MOUSE PRELIMINARY; PRT; 470 AA.  
 AC Q7TMK1  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein A1324046.  
 GN Name=A1324046;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CZECH II;  
 RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore F., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin A.A., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=CZECH II;  
 RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.  
 RC Expression driven by an MMTV-LTR enhancer.;  
 RA Strausberg R.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC055910; AAH55910.1; -; mRNA.  
 DR HSP; P01865; 1KB5.  
 DR GO; GO:0003823; F:antigen binding; IEA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; CI-set; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 KW Hypothetical protein; Immunoglobulin domain.  
 SQ SEQUENCE 470 AA; 51728 MW; 6D90E4DF896BE090 CRC64;  
 Query Match 72.4%; Score 447; DB 2; Length 470;  
 Best Local Similarity 69.4%; Pred. No. 3.6e-36;  
 Matches 84; Conservative 16; Mismatches 17; Indels 4; Gaps 1;  
 QY 1 EIQLOQSGPELVKPGASVOVSKCTGYSTFYNNVYVWQSHGKSLWIGYIDPYNGITY 60  
 Db 20 EVQLQSGPELVKPGASVKISCKASGYTFTGYMHVWQSHGKSLWIGLVNPSNGDTSY 79  
 QY 61 DQNFKGKATLVKSKSTTAFMHLNSLSDSDSAVYFCARDVTVA---LDFWGGTTLTVS 116  
 Db 80 NQKFGKATLVKSKSTTAFMHLNSLSDSDSAVYFCARDVTVA---LDFWGGTTLTVS 139  
 QY 117 S 117  
 Db 140 S 140  
 RESULT 9  
 Q91WR1 MOUSE  
 ID Q91WR1 MOUSE PRELIMINARY; PRT; 488 AA.  
 AC Q91WR1  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Igh-VJ558 protein.  
 GN Name=Igh-VJ558;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FVB/N; TISSUE=Kidney;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore F., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin A.A., Hong L.,



```

GN Name=J558;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C3H/HeJ-lpr/lpr;
RA MEDLINE=96409289; PubMed=8814271;
RX Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gillespie G.S.;
RT "Differences in V kappa gene utilization and VH CDR3 sequence among
RT anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
RL Eur. J. Immunol. 26:2225-2233(1996).
DR EMBL; U59154; AB02916.1; -, mRNA.
DR HSSP; P01751; INQB.
DR SMR; Q8VIJ1; 1-123.
DR Ensemble; ENSMUSG0000057521; Mus musculus.
DR InterPro; IPR007110; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 123
SQ SEQUENCE 123 AA; 13806 MW; CC0037A806E9911E CRC64;

Query Match 71.2%; Score 439; DB 2; Length 123;
Best Local Similarity 69.1%; Pred. No. 5.1e-36;
Matches 85; Conservative 12; Mismatches 20; Indels 6; Gaps 1;

QY 1 EIQLQSGPELVKPGASVQVSKTXGYSTFYNNVVRQSHGKSLWIGYIDPYNGITY 60
   |||||
Db 1 EIQLQSGPELVKPGASVQVSKTXGYSTFYNNVVRQSHGKSLWIGYIDPYNGITY 60
   |||||

QY 61 DONFKGKATLVDSKSTTAFMHLNSLTSDSAVYFCARDV-----TALDFWQGGTTLT 114
   |||||
Db 61 SQKFKGKATLVDSKSTTAFMHLNSLTSDSAVYFCARDV-----TALDFWQGGTTLT 120
   |||||

QY 115 VSS 117
Db 121 VSA 123

RESULT 12
HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A02040; MHMS38.
DR SMR; P01751; INQB.
DR SMR; P06330; 1-118.

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DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 98 V segment.
FT REGION 99 104 D segment.
FT REGION 105 118 J segment.
FT DISULFID 22 96 By similarity.
FT NON_TER 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 70.3%; Score 433.5; DB 1; Length 118;
Best Local Similarity 70.3%; Pred. No. 1.7e-35;
Matches 83; Conservative 13; Mismatches 21; Indels 1; Gaps 1;

QY 1 EIQLQSGPELVKPGASVQVSKTXGYSTFYNNVVRQSHGKSLWIGYIDPYNGITY 60
   |||||
Db 1 EVQLQSGPELVKPGASVQVSKTXGYSTFYNNVVRQSHGKSLWIGIDINPNNGGTSY 60
   |||||

QY 61 DONFKGKATLVDSKSTTAFMHLNSLTSDSAVYFCARDV-TTALDFWQGGTTLTVSS 117
   |||||
Db 61 NQKFKGKATLVDSKSTTAFMHLNSLTSDSAVYFCARDV-TTALDFWQGGTTLTVSS 118
   |||||

RESULT 13
Q20E8_MOUSE PRELIMINARY; PRT; 120 AA.
AC Q920E8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RL Submitted (SRP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307936; AAL09420.1; -, Genomic_DNA.
DR HSSP; P01751; INQB.
DR SMR; Q920E8; 1-120.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 120
SQ SEQUENCE 120 AA; 13204 MW; DC4834AB1DE56F3C CRC64;

Query Match 68.9%; Score 425; DB 2; Length 120;
Best Local Similarity 68.3%; Pred. No. 1.3e-34;
Matches 82; Conservative 14; Mismatches 20; Indels 4; Gaps 1;

QY 1 EIQLQSGPELVKPGASVQVSKTXGYSTFYNNVVRQSHGKSLWIGYIDPYNGITY 60
   |||||
Db 1 EVQLQSGPELVKPGASVQVSKTXGYSTFYNNVVRQSHGKSLWIGIDPYNGTSY 60
   |||||

QY 61 DONFKGKATLVDSKSTTAFMHLNSLTSDSAVYFCARDV-----RDVTTALDFWQGGTTLTVS 116
   |||||
Db 61 NQKFKGKATLVDSKSTTAFMHLNSLTSDSAVYFCARDV-----RDVTTALDFWQGGTTLTVS 120
   |||||

RESULT 14
Q58E61_MOUSE PRELIMINARY; PRT; 485 AA.
AC Q58E61;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)

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DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGC1; 3.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 485 AA; 52628 MW; F08C1FB47C4E44EC CRC64;

Query Match 68.2%; Score 420.5; DB 2; Length 485;
Best Local Similarity 65.6%; Pred. No. 1.7e-33;
Matches 80; Conservative 17; Mismatches 20; Indels 5; Gaps 1;

QY 1 ETQLQSQGPELVKPGASVQVSKTXGYSTFDYNNVYVVRQSHGKSLIEWIGYIDPYNGITY 60
DB 20 EVQLQSQGAEVLKPGASVKISCKASGYTFDNYMDVWKQSHGKSLIEWIGNINPNYDSTIY 79

QY 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDSAVYFCARDVT-----TALDFWGQGLTLTV 115
DB 80 NQKFGKATLTVEKSSSTAYMELRSLTSDSAVYFCARTETTYSYDGGFAYNGRGLTV 139

QY 116 SS 117
DB 140 SA 141

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGC1; 3.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 485 AA; 52628 MW; F08C1FB47C4E44EC CRC64;

Query Match 68.2%; Score 420.5; DB 2; Length 485;
Best Local Similarity 65.6%; Pred. No. 1.7e-33;
Matches 80; Conservative 17; Mismatches 20; Indels 5; Gaps 1;

QY 1 ETQLQSQGPELVKPGASVQVSKTXGYSTFDYNNVYVVRQSHGKSLIEWIGYIDPYNGITY 60
DB 20 EVQLQSQGAEVLKPGASVKISCKASGYTFDNYMDVWKQSHGKSLIEWIGNINPNYDSTIY 79

QY 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDSAVYFCARDVT-----TALDFWGQGLTLTV 115
DB 80 NQKFGKATLTVEKSSSTAYMELRSLTSDSAVYFCARTETTYSYDGGFAYNGRGLTV 139

QY 116 SS 117
DB 140 SA 141

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE LOC367586 protein.
GN Name=LOC367586;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 458 AA; 50161 MW; A0A61DCDD2CA433E CRC64;

Query Match 68.1%; Score 420; DB 2; Length 458;
Best Local Similarity 64.1%; Pred. No. 1.8e-33;
Matches 75; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

QY 1 ETQLQSQGPELVKPGASVQVSKTXGYSTFDYNNVYVVRQSHGKSLIEWIGYIDPYNGITY 60
DB 20 EVQLQSQGAEVLKPGASVKISCKASGYTFDNYMDVWKQSHGKSLIEWIGNINPNYDSTIY 79

QY 61 DQNFKGKATLTVDKSTTAFMHLNSLTSDSAVYFCARDVT-----TALDFWGQGLTLTV 117
DB 80 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYFCARDYFDGYDYGQGVNMTVSS 136
```

Search completed: April 18, 2006, 13:39:33  
Job time : 231 secs

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## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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